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AAY42637;
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			esponse	sponse	thalia	thalia	DZ2AT3	sponse	thalia	thalia	thalia	
	Description		Brassica response	Brassica re	Arabidopsis	Arabidopsis	A. thaliand	Brassica re	Arabidegsis	Arabidopsts	Arabidopsis	
	£					AAG44439	AAY42645	AAY42652	AAG10550	AAG44440	AAG21089	
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ALIGNMENTS

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A nucleic acid encoding a signal transduction protein involved in plant dehiscence, useful for producing shatter resistant male sterile plants
                                                                                    protein; dehiscence; male sterile plant; DZ2 gene; oilseed rape; response regulator protein.
                                                                 Brassica response regulator protein D22.
AAY42637 standard; Protein; 136 AA
                                                                                                                                                                                                                                                          Whitelaw C;
                                                                                                                                                                                          99WO-GB00905.
                                                                                                                                                                                                                98GB-0006113.
                                            10-JAN-2000 (first entry)
                                                                                                                                                                                                                                     (BIOG-) BIOGEMMA UK LID
                                                                                                                                                                                                                                                          Wyatt P, Roberts JA,
                                                                                                                                                                                                                                                                                WPI; 1999-580449/49.
                                                                                        Signal transduction shatter resistance;
                                                                                                                                                                                                                                                                                           N-PSDB; AA222974.
                                                                                                                          Brassica napus
                                                                                                                                               WO9949046-A1.
                                                                                                                                                                                                               20-MAR-1998;
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B. napus DZ2 putative peptide sequence
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99US-0130449.
99US-0130510.
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990S-0131449.
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990S-0134256.
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99US-0134941.
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99US-0128234.
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      sequence represents
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20-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention provides a nucleic acid encoding a signal transduction protein involved in the process of dehiscence. The nucleic acids and proteins are useful for regulating or controlling dehiscence of a pod or an anther in a plant, useful in the production of male sterile plants. The methods, etc. may be used in production of shatter resistance or shatter-delayed plants such as oilseed rape (Brassica napus). The present
                                                                                        The invention provides a nucleic acid encoding a signal transduction protein involved in the process of dehiscence. The nucleic acids and proteins are useful for regulating or controlling dehiscence of a pod or an anther in a plant, useful in the production of male sterile plants. The methods, etc. may be used in production of shatter resistance or shatter-delayed plants such as oilseed rape (Brassica napus). The present sequence represents a B. napus response regulator protein DZ2.
                                                                                                                                                                                                                                                                                                                                                                         1 MATKSMGDIEKIKKKLNVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGS 60
                                                                                                                                                                                                                                                                                                                                                                                                 A nucleic acid encoding a signal transduction protein involved in plant dehiscence, useful for producing shatter resistant male sterile plants
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                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 678; DB 20; Length 136; Best Local Similarity 100.0%; Pred. No. 1e-67; Matches 136; Conservative 0; Mismatches 0; Indels 0
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N-PSDB; AAZ22977.
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AAY 42653

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61 SFDLILMDKEMPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKP 120
                                                                                                                                                                             Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                               1 MATKSMGDIEKIKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGS
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100.0%; Score 678; DB 20;
100.0%; Pred. No. 1e-67;
iive 0; Mismatches 0;
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S-0135353 S-0136529 S-0136621 S-0136732 S-0136732 S-0137728 S-0137728 S-013752 S-0138694 S-013864 S-013864 S-0139115	990S-0139492. 990S-0139492. 990S-0139456. 990S-0139456. 990S-0139459. 990S-0139469. 990S-0139460. 990S-0139460. 990S-0139462. 990S-0139760. 990S-0139750. 990S-0139750. 990S-0139750. 990S-0139763. 990S-0140899. 990S-0140853. 990S-0140853.	0.5 - 0.14215 0.5 - 0.14215 0.5 - 0.14280 0.5 - 0.14284 0.5 - 0.14284 0.5 - 0.14284 0.5 - 0.14284 0.5 - 0.14408 0.5 - 0.14438 0.5 - 0.14438 0.5 - 0.14438 0.5 - 0.14438 0.5 - 0.14438 0.5 - 0.14438 0.5 - 0.14438	10.2 - 0.14488 10.2 - 0.14488 10.2 - 0.14508 10.3 - 0.14508
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                                                                                                                                                                                                                                                                                                                                                                                                                        Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                79.4%; Score 538; DB 21; Length 142; 78.9%; Pred. No. 4.7e-52; ive 8; Mismatches 16; Indels
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                                                                                                                                                                                                                                        AAG44439 standard; Protein; 142 AA
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Matches 112; Conservative
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PR 04-AUG-1999; 99US-0147302.

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PR 20-AUG-1999; 99US-014936.

PR 21-AUG-1999; 99US-014972.

PR 21-AUG-1999; 99US-014972.

PR 22-AUG-1999; 99US-014972.

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PR 22-AUG-1999; 99US-014972.

PR 22-AUG-1999; 99US-0113438.

PR 23-AUG-1999; 99US-0113438.

PR 23-AUG-1999; 99US-0113438.

PR 24-SEP-1999; 99US-0113438.

PR 24-SEP
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The invention provides a nucleic acid encoding a signal transduction protein involved in the process of dehiscence. The nucleic acids and proteins are useful for regulating or controlling dehiscence of a pod or an anther in a plant, useful in the production of male sterile plants. The methods, etc. may be used in production of shatter resistance or shatter-delayed plants such as oilseed rape (Brassica napus). The present sequence represents a DZ2 A. thaliana homologue DZ2AT3 putative peptide sequence.
                                                                                                                                                                                 HRDGGSSFDLILMDKEMPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLN 114
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                                                                            79.4%; Score 538; DB 21; Length 142; 78.9%; Pred. No. 4.7e-52;
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Misc-difference 57
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                                                                                                                                                                                                                                                                                                          55 HRDGGSSFDLILMDKEMPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFWEAGLN 114
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                                                   76.0%; Score 515; DB 20; 76.1%; Pred. No. 1.7e-49; iive 8; Mismatches 20;
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Conservative

Best Local Similarity Watches 93; Conserv

Matches

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80
         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
 21 VDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGVSTT
                                        81 KKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNRCLAKPLIKDKIIPLINQLMDA 136
                                                                                                                                        Arabidopsis thallana protein fragment SEQ ID NO: 8917
                                                                                         AAG10550 standard; Protein; 104 AA
                                                                                                                                                                                                                                                        99US-0121825.
99US-0123180.
99US-0123548.
99US-0125788.
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99US-0138094.
99US-0138540.
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99US-0132486.
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99US-0128234
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99US-0134219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0134221
                                                                                                                        (first entry)
                                                                                                                                                                                         Arabidopsis thaliana
                                                                                                                                                                                                        EP1033405-A2.
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19-APR-1999;
                                                                                                                        17-0CT-2000
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06-APR-1999;
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                                                                                                                                                                                                                         06-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAY - 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-MAY-1999
                                                                                                                                                                                                                                                         25-FEB-1999
                                                                                                                                                                                                                                                                                          25-MAR-1999
                                                                                                         AAG10550;
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                                                                        RESULT 7
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185-0138847 185-0139189 185-0139453 185-0139453 185-0139445 185-0139454 185-0139454 185-0139459 185-0139459 185-0139460 185-0139460	185 0139786 185 0139786 185 0139786 185 014033786 185 014033786 185 014033786 185 014033786 185 014033786 185 014033786 185 014239 185 014239 185 014408 185 014408 185 014433 185 014433	990S-0144352 990S-0144632 990S-0144814 990S-0145086 990S-0145088 990S-0145089 990S-0145089 990S-014524 990S-014524 990S-0145218 990S-0145218 990S-0145218 990S-0145218 990S-0145218 990S-0145218 990S-0145218 990S-0145218 990S-0145218 990S-0145218 990S-0147308 990S-0147308 990S-0147302 990S-0147303 990S-0147302 990S-0147303 990S-0147303 990S-0147303
JUN 1999	0000-1000-1000-1000-1000-1000-1000-100	20 - JUL - 1999; 20 - JUL - 1999; 21 - JUL - 1999; 21 - JUL - 1999; 22 - JUL - 1999; 22 - JUL - 1999; 23 - JUL - 1999; 23 - JUL - 1999; 24 - JUL - 1999; 25 - JUL - 1999; 26 - JUL - 1999; 27 - JUL - 1999; 28 - JUL - 1999; 27 - JUL - 1999; 28 - JUL - 1999; 28 - JUL - 1999; 29 - JUL - 1999; 20 - AUG - 1999; 20 - A
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	Gaps
	Length 104; Indels 0;
	Score 437; DB 21; Pred. No. 5.9e-41; 6; Mismatches 10;
711448888888888888888888888888888888888	64.5%; .larity 84.5%; Conservative
10-Aug-1999; 11-Aug-1999; 13-Aug-1999; 13-Aug-1999; 13-Aug-1999; 14-Aug-1999; 16-Aug-1999; 17-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18-Aug-1999; 18	Query Match Best Local Simila Matches 87; Co
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34 IKAIGGISQTANNGEBAVIHRDGGSSFDLILMDKEMPERDGVSTTKKLREMEVKSMIV 93

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99US-0147303,
99US-0147416,
99US-0147493.
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99US-0148319.
99US-0148341.
     99US-0139453
99US-0139492
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99US-0147302
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05-AUG-1999;
06-AUG-1999;
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11-AUG-1999;
12-AUG-1999;
                                                                                                                                                                                                                                                                                             Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
2 IIKTIGGISQTAKNGEEAVILHRDGEASFDLILMDKEMPERDGVSTTKKLREMKVTSMIV 61
                                  94 GVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLINQLMDA 136
                                                      Arabidopsis thaliana protein fragment SEQ ID NO: 55669.
                                                                                                                                                         AAG44440 standard; Protein; 104 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99005-0121825.
99015-0123180.
99015-0123180.
99015-0123180.
99015-0125788.
99015-01257845.
99015-0129845.
99015-0130147.
99015-0130147.
99015-01301481.
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99015-0130181.
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99US-0139119.
99US-0139452.
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                                                                                                                                                                                                                           18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana.
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11 - MAY - 1999;
14 - MAY - 1999;
14 - MAY - 1999;
14 - MAY - 1999;
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                                                                                                                                                                                           AAG44440;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
       Arabidopsis thaliana protein fragment SEQ ID NO: 23518.
                                                                                                                                      AAG21089 standard; Protein; 70
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30 - APR - 1999
06 - MAY - 1999
05 - MAY - 1999
06 - MAY - 1999
07 - MAY - 1999
11 - MAY - 1999
14 - MAY - 1999
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25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
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19-APR-1999;
21-APR-1999;
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23-APR-1999;
28-APR-1999;
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17-JUN-1999;
18-JUN-1999;
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14-MAY-1999;
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                                                                                          RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 IIKTIGGISQTAKNGEBAVILHRDGBASFDLILMDKEMPERDGVSTTKKLREMKŲTSKIŲ 61
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us-09-646-679-15.rag

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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71 MPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLI 130

131 NQLMDA 136 : | || 61 SHLFDA 66

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PR 27-MD-1999 9998-010066.

PR 27-MD-1999 9998-0110066.

PR 27-MD-1999 9998-011006.

PR 27-MD-1999 9998-011006
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and protein sequences isolated from eucalyptus (Eucalyptus grandis) or pine (Phinus radiate also known as Monterey pine). The protein sequences pine to pine (Phinus radiate also known sequences) or pine (Phinus radiate also known sequences) are involved in cell signalling. The polynucleotide and protein sequences are involved in cell signalling. The polynucleotide and protein sequences can be used to modify the response of plant cells to external signals e.g. environmental changes or pathogens during the growth and suppose to modify cell proliferation, differentiation, elongation and survival, resistance to disease and contrinent metabolism. Examples of modifications which can be produced are altered fruit ripening and senescence of leaves and flowers e.g. to delay senescence of reproductive organs to engineer sterile plants. Other modifications can be used to delay senescence in selected cell types or organs providing fruit and vegetables which have a longer shelf life contents true species giving long stretches of valuable knot-free clear cover and veneers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated polynucleotide encoding a polypeptide involved in cell signaling used for generating transgenic plants with modified responses to external signals ^{\circ}
                                                                         Bucalyptus grandis; Pinus radiata; Monterey pine; plant; modification; plant cell signalling; modulation; transgenic plant; pathogen; growth; environmental change; development; cell proliferation; differentiation; elongation; survival; disease resistance; nutrient metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STIKKLREMEVKSMIVGVISLADNEEERRAFWEAGLNHCLAKPLIKDKIIPLINQ 132
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                                             Pinus radiata cell signalling involved protein SEQ ID NO:127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Page 104-105; 527pp; English.
                                                                                                                                                                                                                                                                                                                                                                     (GENE-) GENESIS RES & DEV CORP LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                     Strabala TJ, Nieuwenhuizen NJ;
                                                                                                                                                                                                                                                                            11-JAN-2000; 2000WO-US00724
                                                                                                                                                                                                                                                                                                                                 99US-0162866
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                (first entry)
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nes 42; Conserv
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                                                                                                                                                                                                         WO200042171-A1
                                                                                                                                                                         Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-JAN-2000
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                27-NOV-2000
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Matches
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The invention provides a nucleic acid encoding a signal transduction protein involved in the process of dehiscence. The nucleic acids and proteins are useful for regulating or controlling dehiscence of a pod or an anther in a plant, useful in the production of male sterile plants. The methods, etc. may be used in production of shatter resistance or shatter-delayed plants such as oilseed rape (Brassica napus). The present sequence represents the partial fragment of B. napus DZ2B protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RscC; antagonist; agonist; cytokinin receptor; receptor; signal transduction; histidine kinase; hormone; cell division; cell differentiation; agriculture; growth regulator; harvest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAT--KSMGDIEK----IKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVI 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A nucleic acid encoding a signal transduction protein involved in plant dehiscence, useful for producing shatter resistant male sterile plants
                                  Signal transduction protein; dehiscence; male sterile plant; DZ2B gene; shatter resistance; oilseed rape; response regulator protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 28.4%; Score 192.5; DB 20; Length 1 Similarity 65.7%; Pred. No. 6.7e-14; 44; Conservative 6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E. coli RscC receiver region of histidine kinase.
         Brassica napus DZ2B partial fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG70785 standard; Protein; 118 AA
                                                                                                                                                                                                                                                              Wyatt P, Roberts JA, Whitelaw C;
                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Fig 5; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-MAR-2002; 2002EP-0005749
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                                                                                                                                                                                                                                 (BIOG-) BIOGEMMA UK LTD
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N-PSDB; AAZ22975.
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Matches 44; Conserv
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                                                                                     Brassica napus.
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                                                                                                                                                                                                        20-MAR-1998;
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                                                                                                                                             30-SEP-1999.
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The invention discloses a method for analysing antagonist or agonist

activity to a cytckinin receptor. The method comprises bringing a
candidate substance into contact with a transformed cell, in which a DNA
candidate substance into contact with a transformed cell, in which a DNA
conciding the receptor has been intraduced, and then measuring the
existence, or the quantity, of the intracellular signal transduction from
the receptor expressed in the cell. The cytchinin receptor comprises an
extracellular region of the receptor, transmembrane regions, a histidine
kinase region and a receiver region of the kinase. The transmembrane
cell division and differentiation of higher plants. The method is used
to cell division and differentiation of higher plants. The method is used
for analysing agonist or antagonist activity to the receptor. A
substance with agonist or antagonist activity to the receptor can be
used, in agriculture, as a plant growth regulator, e.g. after harvest.
The advantage is that the candidate substances do not need to be prepared
in such large amounts as in previous methods and that the method avoids
the immensely long time to observe and evaluate the growth of the plant
and the physicological changes of the plant after spraying. The sequence
presented is the B. coll receiver region of histidine kinase which can
transmit signals to the cytokinin receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 VLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibacterial; PvrR; variant Pseudomonas; microorganism; gram negative; phenotype-mediated antibiotic-resistance; gram-positive; bacterial infection.
                                                                                                                                                                                                           Analyzing agonist or antagonist activity of a substance for use as a plant growth regulator, comprises measuring intracellular signal transduction from a cytokinin receptor expressed in a cell contacted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 STTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKI 126
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Local Similarity 33.9%; Score 171.5; DB 23; Length
Local Similarity 33.9%; Pred. No. 3.2e-11;
Les 37; Conservative 32; Mismatches 37; Indels
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                                                                                                                                                                                                                                                                                                              Disclosure; Page 42; 47pp; English
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                                                                                          (SUMO ) SUMITOMO CHEM CO LID.
          15-MAR-2001; 2001JP-0073812.
29-JUN-2001; 2001JP-0198639.
29-JUN-2001; 2001JP-0198640.
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                                                                                                                                 Higuchi M,
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                                                                                                                                   Kakimoto T,
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16-JAN-2003

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16 LNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERD 75
                                                                                                                                                                                                                                                                                                                            The invention relates to a novel isolated polypeptide comprising a PvrR (variant Pseudomonas) amino acid sequence having at least 50 % identity to a 399 residue amino acid sequence, given in the specification, where expression of the polypeptide, in a microorganism, affects phenotypemediated antibiotic resistance in the microorganism. The methods and compositions of the present invention are useful for the diagnosis, prevention and treatment of gram negative or gram-positive bacterial infection. This sequence repersents a Pseudomonas protein used in the exemplification of the invention.
                                                                                                                                                                                                                       New isolated PvrR polypeptide and polynucleotide that regulates bacterial biofilm formation, useful for the diagnosis, prevention and treatment of gram-negative or gram-positive bacterial infection
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                                              06-JUL-2001; 2001US-303286P.
16-APR-2002; 2002US-373233P.
               05-JUL-2002; 2002WO-US23242
                                                                                                    (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38; Conservative
                                                                                                                                       Drenkard E;
                                                                                                                                                                        WPI; 2003-221608/21.
N-PSDB; AAL55304.
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Best Local Similarity
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ORGANISM: Acinetobacter baumannii
US-09-328-352-7973
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US-09-328-352-7973
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Sequence 31338, A
Sequence 29359, A
Sequence 20355, A
Sequence 36, Appl
Sequence 17557, A
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
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28143, A
220, App
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25128, A
35, Appl
18607, A
27075, A
18, Appl
33, Appl
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198.423 Million cell updates/sec
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                                                                                                                                                                                                       1 MATKSMGDIEKIKKKLNVLI.....LAKPLTKDKIIPLINQLMDA 136
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Sequence 4
Sequence 4
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                                                                                                     August 14, 2003, 16:46:47; Search time 29 Seconds
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-328-352-7973
US-09-252-991A-31338
US-09-252-991A-203959
US-09-252-991A-17557
US-08-843-510B-6
US-08-843-510B-6
US-08-843-510B-3
US-08-843-510B-3
US-08-843-510B-3
US-09-252-991A-28143
US-09-252-991A-26112
US-09-252-991A-26112
US-09-252-991A-26112
US-09-252-991A-27075
US-09-252-991A-27075
US-08-843-510B-3
US-09-252-991A-27075
US-08-843-510B-3
US-09-252-991A-27075
US-08-843-510B-3
US-09-252-991A-18168
US-09-328-310B-3
US-09-328-310B-3
US-09-328-310B-3
US-09-328-310B-3
US-09-328-310B-3
US-09-328-310B-3
US-09-328-310B-3
US-09-328-310B-3
US-09-328-31A-18168
US-09-328-350B-3
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-09-112-450-4
-09-419-291A-4
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                                                                                                                                                                                                                                                                                        328717 seqs, 42310858 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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678
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Perfect score:
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Maximum DB
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Sequence 7973, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTE
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTE
TITLE OF INVENTION: BAUMANII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERRINCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Misuwenhulzen, Miels
TITLE OF INVENTION: Compositions isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE PEREMENE: 11000/1020
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 127
Sequence 6073, Ap
Sequence 22312, A
Sequence 2167, A
Sequence 31677, A
Sequence 23765, Ap
Sequence 114, App
Sequence 16911, A
Sequence 6159, Ap
Sequence 61794, A
Sequence 6746, Ap
Sequence 5430, Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |::|| | ||: || :|: || :|| :|| EATRQLESMGVKTPIVALTA-NTLQSDKDLFFEAGVDDFQSKPLSRDRLVQLLDQ 249
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US-09-328-352-6073
US-09-252-991A-22932
US-09-252-991A-316216
US-09-328-352-6809
US-09-252-991A-23765
US-09-252-991A-23765
US-09-252-991A-23765
US-09-252-991A-23765
US-09-252-991A-16981
US-09-252-991A-16981
US-09-328-364-17904
US-09-328-365-645
US-09-328-365-1779
US-09-328-365-1779
US-09-328-365-1779
US-09-328-352-5430
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US-09-328-352-5430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 127, Application US/09228986 Patent No. 6359198 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
         TYPE: PRT
ORGANISM: Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 42; Conserv
         1188.1
1177.7.0
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COMPUTER READABLE FORM:
SEQ ID NO 29359
LENGTH: 947
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                                                   TYPE: PRT
                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
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APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION. ARENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION. ARENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT PILLION DATE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILLION DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILLING DATE: 1998-02-18
PRIOR FILLING DATE: 1998-02-18
PRIOR FILLING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: MAIC J. RUDEnfield et al.
APPLICANT: MAIC J. RUDEnfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SECUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                674 LHILAVDDHLPNLIVLEALLGELNVKTTKALSGOEALNIIQERIDQKLKPFDLVFMDIQM 733
                                                                                                                                                                                                                   72 PERDGVSTTKKLREM-----EVKSMIVGVT--SLADNEEERRAFMEAGLNHCLAKPLTK 123
                                                                                                                                                                                                                                              868 ARSGVAEVEERKEARALSILLAADHPFNRLTLTMQLESLGHRVTSTEDGEEA--FERWQG 925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||::: | || || : :| || || 326 EDFDVVITDGWMPRWDGYELARRIRSQEALGGRRRCLVIALTASAEKDALERC-LAAGMD 984
                                                                                                                       16 LNVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSS----FDLILMDKEM 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 ATKSMGDIEKIK--KKLNVLIVDDDFLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGG 59
                   Query Match 22.5%; Score 152.5; DB 4; Length 946; Best Local Similarity 30.2%; Pred. No. 3.4e-09; Matches 39; Conservative 34; Mismatches 41; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 22.1%; Score 150; DB 4; Length 1014;
Best Local Similarity 25.5%; Pred. No. 7.4e-09;
Matches 35; Conservative 36; Mismatches 56; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-252-991A-31338
; Sequence 31338, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 29359, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            985 RVLFKPTTLDELARALN 1001
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                                                                                                                                                                                                                                                                                                                     124 DKIIPLING 132
                                                                                                                                                                                                                                                                                                                                                                   791 EQIIQILIO 799
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US-09-252-991A-29359
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LENGTH: 1014
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APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLERC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/4788
PRIOR APPLICATION NUMBER: US/09/4,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'n
                                                                                                                                                                                                                                    689 LLCVDDNPANLLLVQTLLSDLGAQVTAVDSGYAALEVVQRE---RFDLVFMDVQMPGMDG 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 KKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPE 73
                                                                                                                                                                                18 VLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAV-IIHRDGGSSFDLILMDKEMPERDG 76
                                                                                                                                                                                                                                                                                        77 VSTTKKLREMEVKSMI--VGVTSLADN--BEERRAFMEAGLNHCLAKPLTKDKIIPLI 130
                                                                                                                                                                                                                                                                                                                  74 RDGVSTTKKLREMEVKS-----MIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKD 124
                                                                                                                                  8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.7%; Score 147; DB 4; Length 1627; 31.9%; Pred. No. 3.3e-08; tive 26; Mismatches 45; Indels
                                                                           21.8%; Score 148; DB 4; Length 947; 28.8%; Pred. No. 1.1e-08;
                                                                                                                               43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Osmosensing Histidine Kinases
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APPLICANT: Agnan, Jacqueline
APPLICANT: Adnan, Jacqueline
APPLICANT: Alora, Lisa A.
APPLICANT: Simon, Melvin I.
TITLE OF INVENTION: Osmosensing Histidine Kina
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                               33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 20395, Application US/09252991A ; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            United States of America
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GENERAL INFORMATION:
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20395
                                                                                                     Local Similarity 28.8% les 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 31.9%
Matches 37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-09-252-991A-20395
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LENGTH: 1627
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61 SFDLILMDKEMPERDGVSTTKKLREME-----VKSMIVGVTSLADNEEERRAFMEAGLNH 115
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95 EATRLIRREERAQGWPRVPIVALTAHILD--EHRRAGIEAGMDAYLGKPVDRAELYATLE 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 94104
COMPUTER READBALE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,530B
FILING DATE: 16-APR-1997
CLASSIPFCATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                      APPLICANT: Selitrennikoff, Claude
APPLICANT: Agnan, Jacqueline
APPLICANT: Agnan, Jacqueline
APPLICANT: Simon, Melvin I
APPLICANT: Simon, Melvin I
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.6%; Score 139.5; DB 2; 31.1%; Pred. No. 1.8e-07; tive 28; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                      E: Medlen & Carroll, LLP
220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Selitrennikoff, Claude
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 2, Application US/08843530B
; Patent No. 5939306
                                                                                                                                                                                   Sequence 6, Application US/08843530B
Patent No. 5939306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: UTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:11| :: :| |
|1188 YLSKPLQQNHLIQTI 1202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.6%
Best Local Similarity 31.1%
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: no:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                 132 QLM 134
                                                                                         RLL 155
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                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                          RESULT 8
US-08-843-530B-6
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APPLICANT: MARCA J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196-136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17557
LENGTH: 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----VKSMIVGVTS-LADNEEERRAFMEAGLNHCLAKPLTKDKÍTFLÍŇ 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 SSFDLILMDKEMPERDGVSTTKKL-REMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 VLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 DIEKIKKKLNVLIVDDDPLNLIIHEKIIKA---IGGIS--QTANNGEEA---VIIHRDGG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49; Indels
               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,530B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21.2%; Score 144; DB 4; 30.9%; Pred. No. 2.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 21.4%; Score 145; DB 2; Best Local Similarity 29.0%; Pred. No. 3.8e-08; Matches 40; Conservative 40; Mismatches 44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative 28; Mismatches
                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: MACKINGTH, MACKINGTON:
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: UTC-02717
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415,397-8338
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 1220 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.09-252-991A-17557
Sequence 17557, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
                                                                                                     омыек: US/08/843,530в
16-APR-1997
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US-09-252-991A-17557
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TOPOLOGY: not relevant
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Watches 38; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: not
                                                                                                                                           FILING DATE: 16 CLASSIFICATION:
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Floppy disk
       MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 20.6%; Score 139.5; DB 2; Length 1298; Best Local Similarity 31.1%; Pred. No. 1.8e-07; Matches 42; Conservative 28; Mismatches 52; Indels 13; Gaps
APPLICANT: Agnan, Jacqueline
APPLICANT: Alex, Lisa A.
APPLICANT: Alex, Lisa A.
APPLICANT: Alex, Lisa A.
TITLE OF INVENTION: Osmosensing Histidine Kinases
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Median & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Selittennikoff, Claude
APPLICANT: Agnan, Jacqueline
APPLICANT: Alex, Lisa A.
APPLICANT: Simon, Melvin I.
TITLE OF INVENTION: Osmosensing Histidine Kinases
NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.30
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ADDRESSEE: Medien & Carroll, ILP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 4.2.
ATTORNEY/AGENT INPORMATION:
NAME: MACKNIGHT, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: UTC-02717
TELECOMMUNICATION INPORMATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 307-8838
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1298 amino acids
                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,530B
FILING DATE: 16-APR-1997
CLASSIFICATION: 435
                                                                                                                                              STATE: 220 Mouses
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          United States of America
                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Patent No. 5939306
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 not relevant
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1188 YLSKPLQQNHLIQTI 1202
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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US-08-843-530B-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dp
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1075 ATPSLAD---NTKSFEILLAEDNIVNQRLAVKILEKYHHVVIVVGNGEEAVEAVKR---K 1128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 ATKSMGDIEKIKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAV-IIHRDGGS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 20.6%; Score 139.5; DB 2; Length 1298; Best Local Similarity 31.1%; Pred. No. 1.8e-07; Matches 42; Conservative 28; Mismatches 52; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Selttrennikoff, Claude
APPLICANT: Alex, Lisa A.
APPLICANT: Alex, Lisa A.
APPLICANT: Simon, Melvin I.
ITILE OF INVENTION: Osmosensing Histidine Kinases
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSE: ADDRESS:
ADDRESSE: ADDRESS:
CITY: San Francisco
CITY: San Francisco
CITY: United States of America
COUMTRY: United States of America
ZIP: 94104
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,530B
FILING DATE: 16-APR-1997
CLASSIPICATION: 435
                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: MACKIDITL MACKINITON
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: UTC-02717
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415,397-838
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
ATORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: UTC-02717
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/843,530B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 not relevant
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1188 YLSKPLOONHLIGTI 1202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-843-530B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
FILING DATE: 16-APF
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: not
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RESULT 15
US-09-252-991A-26112
; Sequence 26112, Application US/09252991A
                                                                                                                                                                                                                                                                                                                               TYPE: PRT;
CRGANISM: Lactobacillus rhamnosus
US-09-634-238-220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                   Christensson, Anna C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 TKDKI 126
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APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: APPLICATION NUMBER: US/09/252,991A

CURRENT PAPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1999-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-18

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 28143

LENGTH: 1441
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                                                                                                                                                                                                                                                                                                                                                                                                                                               61 SFDLILMDKEMPERDGVSTTKKLREME-----VKSMIVGVTSLADNEEERRAFMEAGLNH 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 LNVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERD 75
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                                                                                                                                                                                                                                                                                                                                                         2 ATKSMGDIEKIKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAV-IIHRDGGS
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                 13;
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20.6%; Score 139.5; DB 4; Length 1441;
Best Local Similarity 28.8%; Pred. No. 2.2e-07;
Matches 34; Conservative 30; Mismatches 43; Indels 11;
                                                                                                                                                                                                                                                                   Query Match 20.6%; Score 139.5; DB 2; Length 1298; Best Local Similarity 31.1%; Pred. No. 1.8e-07; Matches 42; Conservative 28; Mismatches 52; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-252-991A-28143
; Sequence 28143, Application US/09252991A
; Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 220. Application US/09634238
Patent No. 6544772
GENERAL INFORMATION:
APPLICANT: Glenn, Matthew
APPLICANT: Havukkala, 11kka J.
APPLICANT: Blosberg, Leonard, N.
APPLICANT: Lubbers, Mark W.
APPLICANT: Dekker, James
: LLEFAX: (415) 705-8410
: TELEFAX: (415) 397-8338
: INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 1298 amino acids
TYPE: amino acid
STRANDEDNESS: not relent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                   STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECLE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1188 YLSKPLQONHLIQTI 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 CLAKPLTKDKIIPLI 130
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US-09-634-238-220
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RESULT 14
0.90-225-991A-25928

Sequence 25928, Application US/09252991A

Sequence 25928, Application US/09252991A

Setent No. 6551795

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
APPLICATION NUMBER: 0.80/097252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,190

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

WUMBER OF SEQ ID NOS: 33142

SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        670 AILMDCRLPVLDGYSATREIRAGE-NGRQVPIIALTANALQGDRENCLQAGMNDYLAKPF 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 VLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 STIKKLREMEVKSMIVGVISLADNEEERRAFMEAGLNHCLAKPLIKDKIIPLINQL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 DVTCKIREEKIQTPIMILTA-KDNETDKIVGLELGADDYVTKPFSPREIIARIKAI 116
APPLICANT: Holland, Ross
APPLICANT: Holland, Ross
APPLICANT: Croole, Paul W.
APPLICANT: Reid, Julian R.
APPLICANT: Coolbear, Timothy
TITLE OF INVENTION: Polynucleotides, materials incorporating
TITLE OF INVENTION: Polynucleotides, for using them.
FILE REFERENCE: 11000.104301
CURRENT APPLICANTION NUMBER: US/09/634,238
CURRENT FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 422
SOFTWARE: FRASEQ for Windows Version 4.0
SEQ ID NO 220
LENGTH: 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 20.4%; Score 138.5; DB 4; Best Local Similarity 30.2%; Pred. No. 2e-08; Matches 35; Conservative 31; Mismatches 47;
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GENERAL INFORMATION:
APPLICANT: Marc J RUBenfield et al.
APPLICANT: Marc J RUBenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: AERGGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REPRENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NOS: 33142
SEQ ID NO 26112
LENGTH: 860
TYPE: PRT
ORGANISM: PSeudomonas aeruginosa
US-09-252-991A-26112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SFDLILMDKEMPERDGVSTTKKLREM----EVKSMIVGVTSLADNEEERRAFMEAGLNHC 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MATKSMGDIEKIKKKLNVLIVDDDPLNLILHEKIIKAIGGISQTANNGEEAVIIHRDGGS 60
                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

20.0%; Score 135.5; DB 4; Length 860;
Best Local Similarity 26.5%; Pred. No. 3e-07;
Matches 36; Conservative 35; Mismatches 56; Indels 9
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837 LAKPFHRDELKAILDR 852
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Gaps . ف

Search completed: August 14, 2003, 16:51:53 Job time : 30 secs

us-09-646-679-15.rapb

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GenCore version 5.1.6
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OM protein - pr	OM protein - protein search, using sw model
Run on:	August 14, 2003, 16:49:07; Search time 55 Seconds (without alignments) 323.935 Million cell updates/sec
Title: US-	US-09-646-679-15 678

492763 seqs, 131003257 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence: Searched:

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

/ cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/ cgn2_6/ptodata/1/pubpaa/PCTUB_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
/ cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:* 6/ptodata/1/pubpaa/US09_NEW_PUB.pep:* 6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:* 6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:* 'ptodata/1/pubpaa/US10C_PUBCOMB.pep:" /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:* /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:* /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:* Published_Applications_AA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 127, App	Sequence 8, Appli	Sequence 328, App	Sequence 909, App	Sequence 332, App	Sequence 366, App	Sequence 2, Appli	Seguence 7, Appli	Sequence 10049, A	Sequence 4, Appli	Sequence 17, Appl	Sequence 11131, A	Sequence 12532, A	Sequence 9975, Ap	Seguence 13783, A
	QI	US-10-101-464A-127	US-09-918-508-8	US-09-801-368-328	US-10-101-464A-909	US-09-801-368-332	US-09-801-368-366	US-10-126-120-2	US-09-918-508-7	US-10-156-761-10049	US-09-424-951-4	US-10-135-322-17	US-09-815-242-11131	US-10-156-761-12532	US-10-156-761-9975	US-09-815-242-13783
	DB	15	10	10	15	10	10	15	10	15	10	14	σ	15	15	σ
	Ouery Match Length DB	261	118	622	1018	1220	712	974	125	1829	1081	2150	227	203	227	232
æ	Query	29.8	25.3	22.1	21.5	21.4	21.2	20.3	20.2	19.5	18.9	18.8	18.7	18.6	18.5	18.4
	Score	202	171.5	150	146	145	143.5	137.5	137	132	128	127.5	126.5	126	125.5	124.5
	Result No.		7	٣	4	Ŋ	vo	7	80	σ	10	11	12	13	14	15

Sequence 2, Appli	4	Sequence 54, Appl	862	1260	Sequence 956, App	Sequence 12098, A	Sequence 13746, A	Seguence 11629, A	Sequence 10420, A	Sequence 958, App	Sequence 979, App	Sequence 19, Appl	Sequence 2, Appli	Sequence 13096, A	Sequence 114, App	Sequence 11581, A	Sequence 27, Appl	Sequence 10048, A	Sequence 6370, Ap	24,	4, 4	30,	10,	117	827	97		18,	Sequence 10458, A
-11	US-10-116-048	Sn	ns	nS	US	US-09-815-242-12098	CSD	US-09-815-242-11629	US-09-815-242-10420	us	US	OS	us	SD	5 US-10-101-464A-114	ns	ns	ns	ns	ns	SO	ns	SD	ns	Sn	US	US-10-135-3	135-322-18	5 US-10-156-761-10458
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97	247	18	144	248	104	248	218	222	23	89	127	117	117	138	76	24	74	22	23	99	103	10	57	50	81	124	10	109	19
					18.1			17.8							17.0			16.5	16.4							16.2			15.8
124	124	123.5	123	122.5	122.5	122	121.5	120.5	118.5	118	118	117.5	117.5	117	115	114.5	113	112	111.5	111	111	110.5	110	110	110	110	109.5	109.5	107
16	17	60	13	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	გღ	40	4	42	43	44	45

ALIGNMENTS

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US-10.1014-994A-12/
Sequence 127, Application US/10101464A
Sequence 127, Application US/2030046728A1
GENERAL INFORMATION
APPLICANT: Strabala, Timothy
APPLICANT: Higgins, Colleen M.
TILLE OF INVENTION: Colleen M.
TILLE OF INVENTION: and Their Use in the Modification of Plant Cells
FILE REPRENCE: 11000.1202-02
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT APPLICATION NUMBER: US/202-01-01
PRIOR APPLICATION NUMBER: US/28,986
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: 60/162,866
PRIOR FILING DATE: 1999-11-01
PRIOR FILING DATE: 2000-01-12
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
STORY FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SOFTANE: FRASEEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 29.8%; Score 202; DB 15; Length 261; Best Local Similarity 36.5%; Pred. No. 4.4e-14; Matches 42; Conservative 34; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Pinus radiata
US-10-101-464A-127
US-10-101-464A-127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 127
LENGTH: 261
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Gaps

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Sequence 909, Application US/10101464A

Sequence 909, Application US/10101461A

Publication No. US20030046728A1

GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Miggins, Colleen N.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant cell Signaling
FILE REFERENCE: 11000.1020c2
CURRENT APPLICATION NUMBER: US/10/101,464A

CURRENT APPLICATION NUMBER: 09/704,302

PRIOR FILING DATE: 1999-01-12

PRIOR FILING DATE: 1999-01-12

PRIOR FILING DATE: 1999-11-01

SEGURANEE: FastSEQ for Windows Version 4.0

SEGURANEE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           916 DLILMDVCMPVMNGLQATRIIRSFEEMGNWDAAVNAGIELVSSDLSCNGHSSRESKERVP 975
                                                                                                                                                                                                     69 KEMPERDGVSTIKKLREMEVKSMIVGVISLADNEEERRAFMEAGLNHCLAKPLIKDKI-- 126
                                                                                                                                                                                                                                   373 LRKGFHVLLVEDDAVSIQLCSKFLRKYGCTVQVVSDGLSAISTLEKYR----YDLVLMD 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----REMEVKSM 91
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                                                                                                     12 IKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVII---HRDGGSSFDLILMD
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                                                          Indels 20;
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          Length 622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.5%; Score 146; DB 15; Length 10
25.2%; Pred. No. 4e-07;
ive 35; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92 IVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLINQLM 134
        Query Match 22.1%; Score 150; DB 10; Best Local Similarity 28.1%; Pred. No. 7.3e-08; Matches 38; Conservative 32; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 DLILMDKEMPERDGVSTTKKL-------
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US-09-801-368-332
Sequence 332, Application US/09801368
Fatent No. US20020128250A1
GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Call, Brian
APPLICANT: Hecht, Peter
                                                                                                                                                                                                                                                                                                              127 ----- 1PLINQ 132
                                                                                                                                                                                                                                                                                                                                                              487 ILIRYLKDRIPLCEQ 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Eucalyptus grandis
US-10-101-464A-909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
21.5%
Best Local Similarity 25.2%
Matches 41; Conservative
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TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REPRESENCE: 109272.14 (1972)
GURRENT APPLICATION NUMBER: US 09/487,558
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: Patentin version 3.0
                                                                                                                           Sequence 8, Application US/09918508

Sequence 8, Application US/09918508

Sequence 8, Application US20020177162a1

GENERAL INFORMATION:

APPLICANT: KAKIMOTO, TATSUO

APPLICANT: HIGGHI, MASAYUKI

APPLICANT: INOUE, TSUTOMU

TITLE OF INVENTION: TO CYTOKININ RECEPTOR

FILE REFERENCE: Q65478

CURRENT APPLICATION NUMBER: US/09/918,508

CURRENT FILING DATE: 2001-08-01

PRIOR APPLICATION NUMBER: JP 2001-073812

PRIOR FILING DATE: 2001-03-15

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PLEGHIN Ver. 2.1

SEQ ID NO 8: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 ILVVDDHPINRRILADQLGSLGYQCKTANDGVDALNVL--SKNHIDIVLSDVNMPNMDGY 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 VLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV 77
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64 RITQRIRQLGLTLPVIGVTANALABERQRC-LESGMDSCLSKPVTLDVI 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 STTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10; Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 25.3%; Score 171.5; DB 10; Length Best Local Similarity 33.9%; Pred. No. 3.2e-11; Matches 37; Conservative 32; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maxon, Mary
Milno, Todd
No. US20020128250Alman, Thea
Royer, John
Salama, Sofile
Sherman, Amir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 328, Application US/09801368 Patent No. US20020128250A1 GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-801-368-328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Escherichia coli
US-09-918-508-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Busby, Robert
APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-801-368-328
                                                                                                RESULT 2
US-09-918-508-8
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NESCIO-126-120-2
Sequence 2, Application US/10126120
Sequence 2, Application US/10126120
Publication No. US20030108526A1
SENERAL INFORMATION:
APPLICANT: SARAKIDARY: Hitoshi
APPLICANT: Takei, Kentaro
TITLE OF INVENTION: MICROORGANISMS FOR USE IN THE MEASUREMENT OF ENVIRONMENTAL FAC
FILE REPRENDENCE: 111.77-004001
CURRENT APPLICATION NUMBER: US/10/126,120
CURRENT APPLICATION NUMBER: US/10/126,120
CURRENT APPLICATION NUMBER: US/10/126,120
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           556 QLPVLSGIEAAKQIRDFEKQNGIGIQKSLNNSHSNLEKGTSKRFSQAPVIIVALTASNSQ 615
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Patent No. US20020177162A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: RIGHOFF, MASAVUKI
APPLICANT: INOUE, TSUTOMU
APPLICANT: INOUE, TSUTOMU
APPLICANT: TOUE, TSUTOMU
APPLICANT: TOUE, TSUTOMU
APPLICANT: OF INVENTION: ANALYSIS OF AGONIST-ACTIVITY
TITLE OF INVENTION: ANALYSIS OF AGONIST-ACTIVITY
FILE REFERENCE: Q65478
CURRENT APPLICATION NUMBER: US/09/918,508
CURRENT FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-03-15
                                                                                                                                                                        10 EKIKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDK
                                                                                                                       42; Indels 31; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.3%; Score 137.5; DB 15; Length 974; 24.6%; Pred. No. 3.2e-06; Live 32; Mismatches 46; Indels 29;
                                                                       DB 10; Length 712;
                                                                          Query Match 21.2%; Score 143.5; DB 1
Best Local Similarity 27.9%; Pred. No. 4.5e-07;
Matches 39; Conservative 28; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 ERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRA-
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                                                                                                                                                                                                                                                                                       70 EMPERDGVSTTKKLREMEVKS----
                                                                                                                                                                                                                                                                                                                                                                                           102 EEERRAFMEAGLNHCLAKPL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 24.68
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRGANISM: Zea mays US-10-126-120-2
                   US-09-801-368-366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
US-09-918-508-7
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                                                                    APPLICANT: No. US20020128250Alman, Thea
APPLICANT: Royer, John
APPLICANT: Royer, John
APPLICANT: Salama, Sofie
APPLICANT: Sharman, Amir
APPLICANT: Mumbar: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR PILING DATE: 1999-11-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
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TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1136 ENYNMIFMDVQMPKVDGLLSTKMIRRDLGYTSPIVALTAFADDSNIKEC-LESGMNGFLS 1194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 SSFDLILMDKEMPERDGVSTTKKL-REMEVKSMIVGVISLADNEEERRAFWEAGLNHCLA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 DIEKIKKKLNVLIVDDDPLNLIIHEKIIKA---IGGIS--QTANNGEEA---VIIHRDGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
21.4%; Score 145; DB 10; Length 1220;
Best Local Similarity 29.0%; Pred. No. 6.6e-07;
Matches 40; Conservative 40; Mismatches 44; Indels 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR APPLICATION NUMBER: US 09/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: 1999-10-20
PRIOR FILING DATE: 1999-10-20
SEQ ID NOS: 440
SEQ ID NOS: 440
SEQ ID NOS: 420
ILENGTH: 712
TYPE: PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 366, Application US/09801368
Patent No. US20020128250A1
GENERAL INFORMATION
APPLICANT: Busby, Robert
APPLICANT: Healt, Peter
APPLICANT: Healt, Peter
APPLICANT: Maxon, Revin
APPLICANT: Maxon, Mary
APPLICANT: Mine, Todd
APPLICANT: Mine, Todd
APPLICANT: No. US20020128250Alman, Thea
APPLICANT: Salama, Sofie
APPLICANT: Sherman, Amir
APPLICANT: Sherman, Amir
APPLICANT: Sherman, Amir
APPLICANT: Sherman, Amir
                               Maxon, Mary
Milne, Todd
No. US20020128250Alman, Thea
Royer, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | | : : : | | 1195 KPIKRPKLKTILTEFCAA 1212
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  Madden, Kevin
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US-09-801-368-366
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LENGTH: 2150
TYPE: PRT
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US-10-135-322-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 DGVSTTKKLREME--VKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLINQ 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 VLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVII---HRDGGSSFDLILMDKEMPER 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68 DKEMPERDGVSTIKKL-REMEVKSMIVGVISLADNEEERRAFWEAGLNHCLAKPLIKDKI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 LNVLIVDDDPLNLIIHEKIIKA---IGGIS--QTANNGEEA---VIIHRDGGSSFDLILM 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.0;
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                                                                                                                                                                                                                                                                                              Length 125;
                                                                                                                                                                                                                                                                                                                                                                   37; Indels
                                                                                                                                                                                                                                                                                          20.2%; Score 137; DB 10;
29.4%; Pred. No. 2.1e-07;
tive 38; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUBLICATION NO. USEQUINING
GENERAL INFORMATION:
APPLICANT:
IKEDA, HARUO
APPLICANT:
ISHIKAMA, JUN
APPLICANT:
SHIBA, HARUO
APPLICANT:
APPLICANTON:
APPLICANTON:
APPLICANTON:
APPLICANTON:
APPLICANTON:
APPLICANTON NUMBER:
APPLICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10049, Application US/10156761 Publication No. US20030119018A1
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US-09-424-951-4
; Sequence 4, Application US/09424951
; Parent No. US20020137034A1
                                                                                                                                                 TYPE: PRT CRGANISM: Saccharomyces cerevisiae US-09-918-508-7
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Best Local Similarity 31.59
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                  Query Match 20.2%
Best Local Similarity 29.4%
Matches 37; Conservative
NUMBER OF SEQ ID NOS: 22
                                    SOFTWARE: Patentin Ver. SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 KTILTE 124
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US-10-156-761-10049
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2024 RKK--ALIVEDNELNRKVLAQLEKKIDWIISFAENGREA-LKEITGERCFDIVEMDCOMP 2080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 LILMDKEMPERDGVSTTKKLREMEVKS------MIVGVTS---LADNEEERRAFME 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 KKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
18.9%; Score 128; DB 10; Length 1081;
Best Local Similarity 28.3%; Pred. No. 4e-05;
Matches 43; Conservative 31; Mismatches 48; Indels 30; Gaps
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                                    APPLICANT: SOLL, DAVID R.

APPLICANT: SOLL, DAVID R.

TITLE OF INVENTION: CANDIDA ALBICANS TWO-COMPONENT EYBRID KINASE GENE,

TITLE OF INVENTION: CANAILA, AND USE THEREOF

FILE REFERENCE: 087714/0113

CURRENT APPLICATION NUMBER: US/09/424,951

CURRENT FILING DATE: 1998-06-05

PRIOR FILING DATE: 1998-06-06

PRIOR PILING DATE: 1997-06-06

NUMBER OF SEQ ID NOS: 7

SOFTWARE: PATCHIN UNER: 2.1

SOFTWARE: PATCHIN UNER: 2.1

SOFTWARE: PATCHIN UNER: 2.1
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APPLICANT: MACHONEN. AP
APPLICANT: MACHONEN. AM
APPLICANT: RINCHONEN. M
APPLICANT: RINCHONEN. M
TILLE OF INVENTION: WOODEN LEG GENE, PROMOTER AND USES THEREOF
FILE REFERENCE: 5914-086-999
CURRENT PELLING DATE: 2002-04-30
PRIOR FILING DATE: 2000-11-29
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PATENTIN VERSION 3.0
SOFTWARE: PATENTIN VERSION 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        976 KGMDDYVSKPLKPKLLMQTIKKCIHNINQLKE 1007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/10135322; Publication No. US20020173017A1
GENERAL INFORMATION:
APPLICANT: BENREY, PN
APPLICANT: HELARIUTTA, Y
APPLICANT: SRIKANTHA, THYAGARAJAN
APPLICANT: SOLL, DAVID R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Arabidopsis thallana US-10-135-322-17
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Best Local Similarity 32.5'
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) ORGANISM: Candida albicans
US-09-424-951-4
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75 DGVSTTKKLREMEVKSMIVGVTSLAD-------NEEERRAFMEAGLNHCLA 118
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                                                                                                                                                                                                                                                                                                                                                         17 NVLIVDDDPLNLIIHEKIIKAIGGISQ--TANNGEEAVIIHRDGGSSFDLILMDKEMPER 74
                                                                                                                                                                                                                                                                                                                                                                                                        3 SVLVCDDSPLAREALRRAVATVPGVERVTTAANGEE--VLRRWGADRSDLILMDVRMPGL 60
                                                                                                                                                                                                                                                   Length 203;
                                                                                                                                                                                                                                             Ouery Match
18.6%; Score 126; DB 15; Length 20
Best Local Similarity 29.5%; Pred. No. 6.5e-06;
Matches 36; Conservative 20; Mismatches 46; Indels
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29.2%; Pred. No. 8.6e-06;
tive 28; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: INKDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: BHIKAWA, JUN
APPLICANT: SHIRA, TON
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERRECE: 249-262
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR APPLICATION NUMBER: UP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-30
NUMBER OF SEQ ID NOS: 15109
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF, SEQ ID NOS: 15109
SEQ ID NO 12532
LENGTH: 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9975, Application US/10156761 Publication No. US20030119018A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Streptomyces avermitilis US-10-156-761-9975
                                                                                                                                            TYPE: PRT; ORGANISM: Streptomyces avermitilis
US-10-156-761-12532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 18.5%
Best Local Similarity 29.2%
Matches 38; Conservative
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US-10-156-761-9975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 STIKKLREMEVKSMIVGVISLADNEEERRAFMEAGLNHCLAKPLIKDKIIPLINQLM 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 227;
                                                                                                                                                                                                                      APPLICANT: Oblisen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Zyskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yanamoto, Robert T.
TILE OF INVENTION: Prokaryotes
FILLE REFERENCE: ELITRA.011A
CURRENT APPLICANTION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 18.7%; Score 126.5; DB 9; Best Local Similarity 29.1%; Pred. No. 6.7e-06; Matches 34; Conservative 30; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR PILING DATE: 2000-03-21

PRIOR PLING DATE: 2000-03-21

PRIOR PLING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR PILING DATE: 2000-05-26

PRIOR PLING DATE: 2000-10-25

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-12-22

PRIOR PLING DATE: 2001-02-16

NUMBER OF SEC ID NOS: 14110

SOFTHARE: PASSING FOR WINDOWS VETSION 4.0
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APPLICANT: SARAKI, YOSHIYUKI
APPLICANT: HATTORI, MASHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PILLING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
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Sequence 12532, Application US/10156761
Publication No. US2030119018A1
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: IKEDA, HARUO
                                                                                                                     Sequence 11131, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) ORGANISM: Haemophilus influenzae US-09-815-242-11131
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APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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65 ILMDKEMPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLIKD 124
                                                                                                                                                                                                                                        4 EESRKPARVVVADD---QTVVREGIVMLLGLLPGIEVVGAAGDGHEAVKLVAE--LNPDV 58
                                                                                               10 EKIKKKINVLIVDDDPLNLIIHEKIIKAIG---GIS--QTANNGEEAVIIHRDGGSSFDL
DB 15; Length 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
US-09-815-242-13783
; Sequence 13783, Application US/09815242
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GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Oblisen, Rail L.
APPLICANT: Oblisen, Rail L.
APPLICANT: Trawick, John D.
APPLICANT: Ammoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Prokaryotes
FRICA FILLING DATE: 2000-03-21
PRIOR FILLING DATE: 2000-05-23
PRIOR FILLING DATE: 2000-10-23
PRIOR FILLING DATE: 2000-10-23
PRIOR FILLING DATE: 2000-11-27
PRIOR PELICATION NUMBER: 60/265, 308
PRIOR FILLING DATE: 2000-11-27
PRIOR PELICATION NUMBER: 60/265, 308
PRIOR FILLING DATE: 2001-10-21
PRIOR PELICATION NUMBER: 60/265, 308
PRIOR FILLING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SEQ ID NO 13783
MUMBER OF FASTESEQ FOR WINGOWS Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Salmonella typhi
US-09-815-242-13783
Patent No. US20020061569A1
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18 VLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV 77 4 ILLVDDDRELTSLIKELLEMEGFNVLVAHDGEQALELLDD---SIDLLLLDVMPKKNGI 60 78 STTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLINQLM 134 5; Gaps Query Match 18.4%; Score 124.5; DB 9; Length 232; Best Local Similarity 28.2%; Pred. No. 1.1e-05; Matches 33; Conservative 31; Mismatches 48; Indels 5.

Search completed: August 14, 2003, 16:59:18 Job time : 56 secs

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GenCore version 5.1.6
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Copyright (c) 1993 - 2003 Compugen Ltd.	OM protein - protein search, using sw model	August 14, 2003, 16:46:47; Search time 39 Seconds without alignments) as sty willion cell indates sec
	OM protein	Run on:

US-09-646-679-15 678 1 MATKSMGDIEKIKKKLNVLI......LAKPLTKDKIIPLINQLMDA 136 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched: 283308 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

SUMMARIES	Description	histidine kinase h	sensor protein evg	sensor f	probable sensor fo	histidin	sensor protein Rcs	protein	sensor for ctr cap	hypothetical prote	onent	sensory box histid	aerobic respiratio	response regulator	sensor histidine k	two-component hybr	×		sensory box histid	response regulator	sensor histidine k	sensory box histid	response regulator	chemotaxis protein	sensor histidine k	sensory transducti	sensory transducti	aerobic respiratio	-component	cell wall assembly
	QI -	T0887	G6501	A9103	C8587	H876	AD079		C9101	E8586	: AD0149	E8764	AD043	A6948	C8215	AG189	B8725	A3596		G6942	E8219	A8761	25864	G8425	A8726	S7502	S7552	AG090	ABO	A4934
	Length DB	1969		197	197								_	_	736		_	_	_	^,	٠.	_	_	_		_	~	_	939 2	^1
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probable sensor/re aerobic respiratio	aerobic respiratio	aerobic respiratio	sensor/response re	probable two-compo	SLN1 protein - yea	sensor histidine k	sensor histidine k	probable sensor/re	SSK1 protein - yea	sensor histidine k	sensory box histid	sensor protein [im	probable response	two-component regu
A83324 RGECAR	A91140	D85985	E83529	F83153	548387	E87460	C82424	E83212	S64828	C87575	D87559	AI0860	H97516	B41863
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992	778	778	925	1212	1220	560	857	919	712	663	637	918	152	929
22.1	22.1	22.1	21.8	21.7	21.4	21.3	21.2	21.2	21.2	21.1	21.0	21.0	20.9	20.9
149.5	149.5	149.5	148	147	145	144.5	144	144	143.5	143	142.5	142.5	142	142
30	32	33	34	35	36	37	38	36	40	41	42	43	44	45

ALIGNMENTS

RESULT 2

G65010

sensor protein evgS (EC 2.7.3.-) precursor - Escherichia coli (strain K-12)

C;Species: Escherichia coli

C;Date: 10-Sep-1999 *sequence_revision 10-Sep-1999 *text_change 01-Mar-2002

C;Accession: G65010; J00221; I14200

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M., A.; Rose, D.J.; Mau, B.; Shao, Y.

A: Rose, D.J.; Mau, B.; Shao, Y.

Socience 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

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no.vaw.
sensor histidine kinase/response regulator [imported] - Caulobacter crescentus
C; Species: Caulobacter crescentus
C; Species: Caulobacter crescentus
C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001
C; Date: 20-Apr-2001 #sequence_revision 20-Apr-2001
R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
R; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, M.E.; Eaft, D.H.; Ko
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
Proc. Natl. Acad. Sci. U. S.A. 98, 4136-4141, 2016
A; Status: Dreliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-394 <STO>
A; Cross-references: GB:AE005673; NID:g13424832; PIDN:AAK25124.1; GSPDB:GN00148
A; Genetics:
A; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable sensor for regulator EvgA evgS [imported] - Escherichia coli (strain 0157:H7 probable sensor for regulator EvgA evgS [imported] - Escherichia coli (strain 0157:H7 c; Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 #sequence_revision 165879 #text_change 14-Sep-2001 #sequence_revision 165879 #text_change 14-Sep-2001 #sequence 265879 #text_change 14-Sep-2001 #text_change 14-Sep-2001 #text_change 15-Sep-301 #text_change
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                                                 72 PERDGYSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLIN 131
                                                                                                                                         72 PERDGYSTIKKLREMEVKSMIVGYTSLADNEEERRAFMEAGLNHCLAKPLIKDKIIPLIN 131
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          12 IKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: evgS
C;Superfamily: evgS protein; response regulator homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 176.5; DB 2; Pred. No. 7.5e-07; 25; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 174;
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Best Local Similarity 34.4%;
Matches 42; Conservative 2
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              probable sensor for regulator EvgA [imported] - Escherichia coli (strain 0157:H7, substract Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 24-Aug-2001
C;Date: 18-Jul-3001 #sequence_revision 18-Jul-2001 #text_change 24-Aug-2001
C;Date: 18-Jul-3001
B;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
By Res. 8, 11-22, 2001
By Hayashi T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Researce number: A9629; MUD:21156231; PMID:11258796
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule`type: DNA^A
A;Residues: 1-1197 (4Mx>
A;Cross-references: GB:BAQ00007; PIDN:BAB36672.1; PID:g13362719; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 72 PERDGVSTTKKLREMEVKSMIVGVTSLADNEBERRAFMEAGLNHCLAKPLTKDKIIPLIN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 IKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEM 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.0%; Score 176.5; DB 2; Length 1197; glocytic 34.4%; Pred. No. 7.5e-07; Conservative 25; Mismatches 52; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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α
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Superfamily: evgS protein; response regulator homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
'Aba 42; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1072 QL 1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 QL 133
A; Accession: G65010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECs3249
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Matches
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A; Title: RcsB and RcsC: a two-component regulator of capsule synthesis in Escherichia A; Reference number: JV0068; MUID:90130299; PMID:2404948
A; Accession: JV0069
A; Accession: JV0069
A; Accession: JV0069; MUID:90130299; PMID:2404948
A; Residues: 1-12, /16, /115-918, /s', 920-933 <STO>
A; Reperimental source: strain R12
A; Bacteriol. 175, 5384-5394, 1993
A; Reference number: A48659; MUID:93374832; PMID:8366025
A; Reference number: A48659; MUID:93374832; PMID:8366025
A; Residues: 1-112, /16, /15-298, /v', 300-759, 'E', 761-873, 'T', 875-921, 'V', 923-931, 'E', 93
A; Residues: 1-112, '16', 115-298, 'v', 300-759, 'E', 761-873, 'T', 875-921, 'V', 923-931, 'E', 93
A; Residues: 1-112, '16', 115-298, 'v', 300-759, 'E', 761-873, 'T', 875-921, 'V', 923-931, 'E', 93
A; Reperimental source: strain R30 (09:R30:H12)
C; Comment: This protein acts as the sensor of the two-component regulatory system to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A) Gene: rosc

A) Map position: 48 min

C) Superfamily: rosc protein; response regulator homology

C) Superfamily: rosc protein; capsule synthesis; phosphohistidine; phosphoprotein;

C) Reywords: autophosphorylation; capsule synthesis; phosphohistidine; phosphoprotein;

F; 4-26/Domain: transmembrane #status predicted <TM1>

F; 98-318/Domain: transmembrane #status predicted <TM2>

F; 911-920/Domain: response regulator homology <RRH>

F; 463/Binding site: phosphate (His) (covalent) #status predicted

F; 859/Binding site: phosphate (Asp) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        าธ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-933 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB36530.1; PID:g13362576; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 VLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 STTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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C;Superfamily: rcsC protein; response regulator homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 25.3%; Score 171.5; DB 1; Best Local Similarity 33.9%; Pred. No. 1.5e-06; Matches 37; Conservative 32; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.3%; Score 171.5; DB 2
33.9%; Pred. No. 1.5e-06;
tive 32; Mismatches 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 33.99
Matches 37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 8
C91017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Another this species has also been called Salmonella enterica subsp. enterica serova C. Species: Salmonella enterica subsp. enterica serovar Typhi
A,Note: this species has also been called Salmonella typhi
C,Species: Date: John Species has also been called Salmonella typhi
C,Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C,Accession: AD0790
C,Gaora, P.: Cronin, A.: Davis, P.: Davies, R.M.: Dowd, L.: White, N.: Farrar,
C, S.: Moule, S.: O'Gaora, P.
A,Authors: Parry, C.: Quail, M.: Rutherford, K.; Simmonds, M.: Skelton, J.: Stevens, K.;
A,Tille: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A; Accession: AD0790
A; Accession: AD0790
A; Status: Preliminary
A; Accession: AD0790
A; Status: Preliminary
A; Accession: AD0790
A; Residues: 1-948 <-Par>
A; Residues: 1-948 <-Par>
A; Coss-references: GB:AL513382; PIDN:CAD07502.1; PID:g16503497; GSPDB:GN00176
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R;Stout, V.; Gottesman, S.
J. Bacteriol. 172, 659-669, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sensor protein rcsc (EC 2.7.3.-) - Escherichia coli (strain K-12)
Nyllernate names: regulatory protein rcsc
G.Species: Escherichia coli
G.Species: Escherichia coli
C.Date: 30-Jun-1991 #sequence_revision 17-Oct-1997 #text_change 01-Mar-2002
G.Accession: H64991, 700069; A48659
R.Blatcher, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A.Title: The complete genome sequence of Escherichia coli K-12.
A; Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                            827 ILVVDDHPINRRLLADQLGSLGYQCKTANDGVDALNVL--SKNAIDIVLSDVNMPNMDGY 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-933 <BLAT>
                                                                                                                                                                                                                                                                 74 RDGVSTTKKLREMEVKSMIVGVTSLADNEE--ERRAFMEAGLNHCLAKPLTKDKIIPLIN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 VLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV 77
                                                                                                                                  73
                                                                                                                                      14 KKLNVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A)Gene: rosC
C;Superfamily: rcsC protein; response regulator homology
C;Keywords: phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.6%; Score 173.5; DB 2; 33.9%; Pred. No. 1e-06; tive 33; Mismatches 36;
       Pred. No. 3.4e-07;
                                                                      31; Mismatches
                                   31.7%;
                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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tes 37; Conserv
                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           OLM 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       380 SLL 382
                                                                             39;
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Best Loc Matches

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C; Genetics:

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Gispecies: Yersinia pestis
Gispecies: Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
Giscession: AD0432
Riperinil, J.; Wren. B. W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M. Ararkhill, J.; Wren. B. W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M. Aenstraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G. 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel Nature 413, 53-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586350
                                                            Cispecies: Caulobacter crescentus
Cipate: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
Cipate: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
Cipates 20-Apr-2001 #sequence_revision 20-Apr-2001
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, B.; Laub, M.T.; DeBopy, R.T.; Dodson, R.J.; Duxkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko n. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A; Felerence number: As7249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: arcB
C;Superfamily: aerobic respiration control sensor protein arcB; response regulator ho
C;Reywords: phosphotransferase
                            sensory box histidine kinase/response regulator [imported] - Caulobacter crescentus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-778 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC92784.1; PID:g15981477; GSPDB:GN00175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 24.0%; Score 162.5; DB 2; Length 642; Best Local Similarity 33.0%; Pred. No. 5.5e-06; Matches 36; Conservative 28; Mismatches 40; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-642 <STO>
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                                                                                                                                                                     A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-references: GB: AE005174; NID: 912516556; PIDN: AAG57353.1; GSPDB: GN00145; UWGP: 234
A; Experimental source: strain 0157: H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                two component sensor kinase/response regulator protein RcsC (EC 2.7.3..) [imported] - Ye
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C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C;Accession: ADO149
C;Accession: ADO149
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice; M.B., Genc-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Attle: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
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A;Molecule type: DNA
A;Residues: 1-957 <KUR>
A;Residues: 1-957 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC90055.1; PID:g15979276; GSPDB:GN00175
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869 RLTQRIRQLGLTLPVIGVTANALAEEKQRC-LESGMDSCLSKPVTLDVI 916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 25.3%; Score 171.5; DB 2; Length 933; Best Local Similarity 33.9%; Pred. No. 1.5e-06; Matches 37; Conservative 32; Mismatches 37; Indels 3
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C;Superfamily: rcsC protein; response regulator homology
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C;Superfamily: rcsC protein; response regulator homology
C;Keywords: phosphotransferase
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RESULT 10

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RESULT 11

Db Q_{λ} q

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Search completed: August 14, 2003, 16:51:17
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Best Local Similarity 27.77
Matches 39; Conservative
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A;Residues: 1-736 <HEI>
A;Cross-references: GB:AE004259; GB:AE003852; NID:g9656353; PIDN:AAF94979.1; GSPDB:GN001
A;Experimental source: serogroup 01; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC1831
response regulator homolog - Archaeoglobus fulgidus
C.Species: Archaeoglobus fulgidus
C.Species: Archaeoglobus fulgidus
C.Species: Archaeoglobus fulgidus
C.Species: O5-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 03-Mar-2003
C.Socosabion: A69487
R.Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
C.Stelschmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Alile: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed
A;Reference number: A69250; MuID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Staus: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA B;Molecule type:
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C;Decies: Vibrio cholerae
C;Decies: Vibrio cholerae
C;Decies: Vibrio cholerae
C;Decession: C82151
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.
R;Heidelberg, J.F.; Eisen, J.A.; Venter, J.C.; Fraser, C.M.
I, R.N.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.5%; Score 159; DB 2; Length 117
28.3%; Pred. No. 1.5e-06;
ive 42; Mismatches 31; Indels
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Best Local Similarity 30.8%
Matches 41; Conservative
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Best Local Similarity 28.35
Matches 36; Conservative
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V, ACCESSION: NALESY,

MAKAZAKI, N.; SHAMMURA, Y.; WOLK, C.P.; KURILZ, T.; Sasamoto, S.; Watanabe, A.; Irigu
NAKAZAKI, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata
DNA Res. 8, 205-213, 2001

A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium
A,Reference number: AB1807; MUDD:21595285; PMID:11759840

A,Recession: AG1897

A,Stellusi prealiminary
A,Stellusinary
A,Residues: 1-1645 <KUR>
A,Residues: 1-1645 <KUR>
A,Cross references: GB:BA000019; PIDN:BAB72686.1; PID:g17130074; GSPDB:GN00179
A,Cross references: strain PCC 7120
C,Genetics:
A,Genetics:
A,Genetics:
A,Genetics: al10729
                                                                                                                                                                                                              two-component hybrid sensor and regulator all0729 (imported) - Nostoc sp. (strain PCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Nostoc sp. PCC 7120
A;Notes Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C;Accession: AG1897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 DLILMDKEMPERDGVSTTKKLREMEVK-----SMIVGVTSLADNEEERRAFMEAGL 113
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120 PLTKDKIIPLING 132
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Q8x613 escherichia P10957 escherichia 034534 bac11lus su Q4594 caulobacter P1244 escherichia Q44006 alcaligenes P49246 xanthomonas C56312 thermotoga P51358 porphyra pu P43501 pseudomonas Q0606 escherichia O78428 guillardia

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Utsumi R., Katayama S., Ikeda M., Igaki S., Nakagawa H., Miwa A., Taniguchi M., Noda M.;
"Cloning and sequence analysis of the evgAS genes involved in signal transduction of Escherichia coli K-12.";
Nucleic Acids Symp. Ser. 27:149-150(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=K12;
MEDLINE-97349980; PubMed=9205837;
MEDLINE-97349980; PubMed=9205837;
MEDLINE-97349980; Miba T., Isono K.,
Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kato A., Ohnishi H., Yamamoto K., Furuta E., Tanabe H., Utsumi R., "Transcription of emrKY is regulated by the EvgA-EvgS two-component system in Escherichia coli K-12.", Biosci. Biotechnol. Biochem. 64:1203-1209(2000).
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SEQUENCE FROM N.A.
STARAIN-RIZ / Mal555,
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.:
                                                                                                                                                                                                                                                                                             Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                        STRAIN=K12;

MEDIJRE-94171083; PubMed-8125343;
UtSuni R., Katayama S., Taniguchi M., Horie T., Ikeda M., Igaki Sukagawa H., Miwa A., Tanabe H., Noda M.;
Newiy dentifixed genes involved in the signal transduction of Escherichia coli K-12.";
Gene 140:73-77(1994).
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Science 277:1453-1474(1997).
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                                                                                                                                                                                                               EVGS_ECOLI STANDARD; PRT; 1197 AA. BY0855; P77644; Q9RE36; Q9RE37; 01-JUL-1993 (Rel. 26, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 28-FBD-2003 (Rel. 41, Last annotation update) ENGS OR B2370.
                                                                                                                                                            ALIGNMENTS
ZEAR_ECO57
WREL_ECOLI
CITT_BACSU
CIFRA_CAUCE
CPKR_ECOLI
CREATERA
ATOC_ECOLI
                                                                                                                            YC27_GUITH
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MEDLINE=20378313; PubMed=10923791;
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MEDLINE=93173621; PubMed*1289796;
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1117.5
1112.5
111.5
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EVGS_ECOLI
   Q56128 salmonella
P58662 salmonella
P14376 escherichia
P18769 myxococcus
P38889 saccharomyc
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bacillus su
bacillus ha
bacillus su
bordetella
bacillus me
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eschérichia
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klebsiella
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278.071 Million cell updates/sec
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                                                                                                                                                     1 MATKSMGDIEKIKKKLNVLI......LAKPLTKDKIIPLINQLMDA 136
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P96126
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P14375
                                                                                 August 14, 2003, 16:46:47; Search time 23 Seconds
                GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                    hits satisfying chosen parameters:
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SSK1_YEAST
GACS_PSESY
DCTR_BACSU
DCTR_BACHD
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BVGS_BORPE
DCTR_BACME
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YSO1_PLEBO
BARA_SHIFL
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ZRAR_ECOLI
ALGR_PSEAE
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BVGS_BORBR
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CHEY_TREPA
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RCSC_SALTI
RCSC_SALTY
RCSC_ECOLI
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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678
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                                                                                                                                                                                                                                 Perraud A.-L., Kimmel B., Weiss V., Gross R.;

Perraud A.-L., Kimmel B., Weiss V., Gross R.;

Perraud A.-L., Kimmel B., Weiss V., Gross R.;

Specificity of the BugAs and EvgAs phosphorelay is mediated by the "Specificity of the BugAs and EvgAs phosphorelay is mediated by the C-terminal HPt domains of the sensor proteins.";

Mol. Microbiol. 27:875-887(1998).

-!- FUNCTION: Member of the two-component regulatory system evgS/evgA. Phosphorylates evgA via a four-step phosphorelay in response to environmental signals.

-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasundaram S., Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C., Yamagata S., Horiuchi T., "Construction of a contiguous 874-kb sequence of the Escherichia coli - K12 genome corresponding to 50.0-68.8 min on the linkage map and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --- PTM: Activation requires a sequential transfer of a phosphate group from a His in the primary transmitter domain, to an Asp in the receiver domain and to a His in the secondary transmitter
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InterPro; IPR00189; Response_reg.

InterPro; IPR00189; Response_reg.

InterPro; IPR00181; SBP_glu_receptor.

InterPro; IPR00181; SBP_glu_receptor.

InterPro; IPR00181; SBP_glu_receptor.

Pfam; PF00512; H38RA; I.

R Pfam; PF00497; SBP_bac_3; I.

R PRINTS; PR00497; SBP_bac_3; I.

R PRART; SM00389; H3RA; I.

R SMART; SM00089; H3RA; I.

R SMART; SM00062; PBPD; 2.

R PROSITE; PS50109; HIS_KIN; I.

R SMART; SM0048; PRC; I.

R PROSITE; PS50109; HIS_KIN; I.
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CYTOPLASMIC (POTENTIAL).
POTENTIAL.
PERIPLASMIC (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Contains 1 histidine kinase domain.
-!- SIMILARITY: Contains 1 HPT domain.
-!- SIMILARITY: Contains 1 response regulatory domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR003594; ArPbind_ATPase.
InterPro; IPR0043598; Bact_Sene_Pr_C.
InterPro; IPR003661; His_KinA.
InterPro; IPR005467; His_KinAse.
                                                                                                                                  analysis of its sequence features.";
DNA Res. 4:91-113(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF201840; AAF17563.1; -.
EMBL; AF201841; AAF17564.1; -.
EMBL; AE000325; AAC75429.1; -.
EMBL; D90867; BAA16241.1; -.
PIR; G65010; G65010.
HSSP; P06143; 1UDR.
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CHARACTERIZATION.
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72 PERDGVSTIKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLIKDKIIPLIN 131
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STRAIN-0157:H7 / RIMD 0509952;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 IKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEM
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SEQUENCE FROM N.A.
STAIR—1217:147, EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Perna N.T., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Melch R.A., Blattner F.R.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                  26.3%; Score 178.5; DB 1; Length 1197; 34.4%; Pred. No. 2.9e-07;
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CYTOPLASMIC (POTENTIAL).
                                         RESPONSE REGULATORY.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Sensor protein evgS precursor (EC 2.7.3.-).
Escherichia coli 0157:H7.
                    HISTIDINE KINASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 42; Conservative
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1074 107
1197 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1072 QL 1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QL 133
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PERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLIN 131
       72
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                                                                                                                                                     RESULT 3
RCSC_SALTI
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                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
       Res. 8:11-22(2001). FUNCTION: Member of the two-component regulatory system evgS/evgA. Phosphorylates evgA via a four-step phosphorelay in response to environmental signals (By similarity). SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
W; A01055089D9618E2 CRC64,
                                                                                                    -: PTM: Activation requires a sequential transfer of a phosphate group from a His in the primary transmitter domain, to an Asp in the receiver domain and to a His in the secondary transmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SENSOITE, PSSOILO, RESPONSE_REGULATORY; 1. Sensory transduction; RESPONSE_REGULATORY; 1. Phosphorylation; SIGNAL 1 21 SENSOR PROTEIN EVGS. CHAIN 22 1197 SENSOR PROTEIN EVGS. CYTOPLASMIC (POTENTIAL). TRANSMEM 326 POTENTIAL. POTENTIAL. DOMAIN 316 POTENTIAL. DOMAIN 318 558 POTENTIAL.
                                                                                                                                                       domain (By similarity).
--- SMILARITY: Contains 1 histidine kinase domain.
--- SIMILARITY: Contains 1 HPT domain.
--- SIMILARITY: Contains 1 response regulatory domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HISTIDINE KINASE.
RESPONSE REGULATORY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.0%; Score 176.5; DB 1
34.4%; Pred. No. 4.3e-07;
tive 25; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR0043594; ATPbind_ATPase.
InterPro; IPR004358; Bact_sens_pr_C.
InterPro; IPR004661; His_Kina.
InterPro; IPR004667; His_Kinase.
InterPro; IPR00467; His_Kinase.
InterPro; IPR001789; Response_reg.
InterPro; IPR001311; SBP/glu_receptor.
InterPro; IPR001311; SBP/glu_receptor.
InterPro; IPR001311; SBP/glu_receptor.
InterPro; IPR001311; SBP/glu_receptor.
InterPro; IPR00131; SBP_bac_3.
Pfam; PF00512; HisRA; 1.
Pfam; PF00072; response_reg; 1.
Pfam; PF00072; response_reg; 1.
PRIMS; PR00044; BCTRLSENSOR.
Probom; PD000039; Response_reg; 1.
SWART; SM00073; HPT; 1.
SWART; SM00073; HPT; 1.
SWART; SM00073; HPT; 1.
SWART; SM000448; REC; 1.
PROSITE; PS50044 HPT, 1.
PROSITE; PS50044 HPT, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134953 MW;
                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE005468; AAG57495.1; -. EMBL; AP002561; BAB36672.1; -. PIR; A91035; A91035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1197
721
1009
1137
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                                                                                           (Probable).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Sim.
42;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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1013 PNVDGFELTRKLREQNSSLPIWGLTANA-QANEREKGLNCGMNLCLFKPLTLDVLKTHLS 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=TV2 / ATCC 700931;
MEDLINE=22531377; PubMed=12644504;
MEDLINE=22531377; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- PTM: Activation probably requires a transfer of a phosphate group between a His in the transmitter domain and an Asp of the receiver domain (By similarity)
-:- SIMILARITY: Contains 1 histidine Kinase domain.
-:- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
-:- SIMILARITY: Contains 1 response regulatory domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Bacteriol. 178:1691-1698(1996).

-i. FUNCTION: Member of the two-component regulatory system rcsC/rcsB intolved in the regulation of the expression of genes involved in colanic acid capsule synthesis. RcsC probably functions as a membrane-associated protein kinase that phosphorylates rcsB in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Parkhill J. Douger D. James K.D., Thomson N.R., Pickard D., Wain J Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Brooks K., Chillingworth T., Connerton P., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Simmonds M., Skelton J., Stevens K., Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CTIB",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-TY2 / ATCC 700931, MEDLINE-96198173; PubMed-8626298; ATCO 700931, ATCO 70093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              response to environmental signals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Protecobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Sensor protein rcsC (EC 2.7.3.-) (Capsular synthesis regulator
                                                                                                                                                                                                                                                                                                                             948 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteriol. 185:2330-2337(2003).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           component C).
RCSC OR STY2496 OR T0594.
                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella typhi
                                                                                                                                                 1072 QL 1073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=601;
                                                                              132 QL 133
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                                                                                                                                                                                                                                                                                                                                 RCSC_SALTI
Q56128;
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ä

3; Gaps

52; Indels

Conservative

Similarity

Best Loc Matches

δ Dp

12 IKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEM 71

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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 VLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       827 ILVVDDHPINRRLLADQLGSLGYQCKTANDGVDALNVL--SKNAIDIVLSDVNMPNMDGY 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          940 RESPONSE REGULATORY.
979 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
975 PHOSPHORYLATION (BY SIMILARITY).
106237 MW; ASSA217012654865 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                               Sensory transduction; Transferase; Kinase; Bacterial capsule;
Inner membrane; Transmembrane; Phosphorylation; Complete proteome.
DOMAIN 1 20 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      78 STIKKLREMEVKSMIVGVISLADNEEERRAFMEAGLNHCLAKPLIKDKI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PERIPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.6%; Score 173.5; DB 1; 33.9%; Pred. No. 5.9e-07; tive 33; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HISTIDINE KINASE
                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50112; PAS; FALSE_NEG.
PROSITE; PS50110; RESPONSE_REGULATORX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                    InterPro: IPR003594; ATPbind APPase.
InterPro: IPR00458; Bact_sens_pr_C.
InterPro: IPR004661; His_kinA.
InterPro: IPR005467; His_kinase.
InterPro: IPR000149; PAS_domain.
InterPro: IPR001789; Response_reg.
                                                                                                                                                                                                                                                                Pfam, PF00072; response_reg; 1.
PRINTS; PR00344; BCTRLSENSOR.
Prodom; PD000039; Response_reg; 1.
SMART; SM00387; HarPase_c; 1.
SMART; SM00388; HisKA; 1.
                                                                         EMBL; AL627274; CAD07502.1; -. EMBL; AE016836; AA068299.1; -.
                                                                                                                                                                                                                                  Pfam; PF02518; HATPase_c; 1.
Pfam; PF00512; HiskA; 1.
                                                                                                        EMBL; X87830; CAA61095.1; -. HSSP; P06143; 1UDR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         948 AA;
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es 37; Conserv
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MOD_RES
MOD_RES
SEQUENCE
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DOMAIN
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948 AA;
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MOD_RES
SEQUENCE
                                                                                                                                      Query Match
Best Local
DOMAIN
                                         DOMAIN
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                                                                                                                                                                                                                                                                                              STRAIN=LT2 / SGSC1412 / ATCC 700720;

MEDINE=21534948; Pubmed=11677609;

MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille-P.,

Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
                                                                                                                                                                                                Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Sensor protein rosC (EC 2.7.3.-.) (Capsular synthesis regulator
                   948 AA.
                   PRT;
                   STANDARD;
                                                                                                                                                                             Salmonella typhimurium.
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                       STM2271
                                                                                                                                                                                                                                            NCBI_TaxID=602;
                 RCSC_SALTY
P58662;
                                                                                                                                        component C)
                                                                                                                                                            RCSC OR
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RCSC_SALTY
TD RCSC_SS
AC 7866_SS
DT 28-FEB
DT 18-FEB
DT 18-FEB
DT 000000
CS Salmon
CN CSC 0
CS Bacter
CO Bacter
CO NCBL_T
RN 181
RN 181
RN 181
RN 181
RN SEQUEN
RX MEDLIN
RA MEDLIN
RA COUTCH

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 VLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV 77
                                                                                                                                                                                                                               between a His in the transmitter domain and an Asp of the receiver domain (By similarity)

-: SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.

-: SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.

-: SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
                                                                                                Nature 413:852-856(2001).

-i-FUNCTION: Member of the two-component regulatory system rcsC/rcsB involved in the regulation of the expression of genes involved in colanic acid capsule synthesis. RcsC probably functions as a membrane-associated protein kinase that phosphorylates rcsB in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       940 RESPONSE REGULATORY.
719 PHOSPHORYLATTON (AUTO-) (BY SIMILARITY).
775 PHOSPHORYLATION (BY SIMILARITY).
106279 MW; BAAADBDAS57D5868B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; "Complete genome sequence of Salmoneila enterioa serovar Typhimurium LT2.";
                                                                                                                                                                                response to environmental signals.
SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SMO0448; NEC. 1.
PROSTER; PS50109; HIG_KIN; 1.
PROSITE; PS50110; PAS; FALSE_NEG.
PROSITE; PS50110; RESPONSE_REGULATORY; 1.
Sensory transduction; Transferase; Kinase; Bacterial capsule;
Sensory transduction; Transferase; Kinase; Bacterial capsule;
Inner membrane; Transmembrane; Phosphorylation; Complete proteome.

CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                78 STIKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLIKD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE008801; AAL21172.1; --.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWART; SW00387; HATPASE_C; 1.
SWART; SW00388; HisKA; 1.
SWART; SW00448; REC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37; Conservative
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us-09-646-679-15.rsp

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777
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EMEL: L11272; AAA24505.1; ALT_INIT.
EMBL: AAG000311; AAG75278 1, ALT_INIT.
EMBL: D90850; BAA16001.1; ALT_FRAME.
EMBL: D90851; BAA16006.1; ALT_FRAME.
EMBL: D90851; BAA16009.1; ALT_FRAME.
EMBL: D90851; BAA16014.1; ALT_FRAME.
HSSP; P06143; IUDR.
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335
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479
875
315
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935
949 AA;
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Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                                                                                                           EcoGene; EG10822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FRZE_MYXXA
P18769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRANSMEM
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MOD_RES
MOD_RES
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VARIANT
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SO THE PROPERTY OF THE PROPERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Itoh T., Alba H., Baba T., Fullita K., Hayashi K., Inada T., Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Moroni H., Mori H., Moroni T., Motomura K., Nakade S., Makamura Y., Ashimoto H., Nishio Y., Oshima T., Saito N., Sampel G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Yamanoto Y., Horiuchi T., Takeda J., Takemoto K., Wada C., Tamanoto Y., Horiuchi T., Takeda J., Takemoto K., Wada C., Tamanoto Y., Horiuchi T., Takeda J., Takemoto K., Wada C., Tamanoto Y., Horiuchi T., Takeda J., Takemoto K., Wada C., Takemoto Y., Horiuchi T., Takeda J., Takemoto K., Wada C., Takemoto C., Polo Min region on the linkage map."; DNA Res. 3:379-322(1996).

I. DNA Res. 3:379-322(1996).

I. DNA Res. 3:379-322(1996).

I. Involved in the regulation of the expression of genes involved in colanic acid capsule synthesis. ResC probably functions as a membrane-associated protein kinase that phosphorylates rcsB in response to environmental signals.

C. -: Subschildar Location: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probable).

--- PTM: Activation probably requires a transfer of a phosphate group between a His in the transmitter domain and an Asp of the receiver domain (By similarity).
--- SIMILARITY: Contains 1 histidine kinase domain.
--- SIMILARITY: Contains 1 PAS (PER-ARMT-SIM) dimerization domain.
--- SIMILARITY: Contains 1 PAS (PER-ARMT-SIM) dimerization domain.
--- SIMILARITY: Contains 1 response regulatory domain.
--- CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 808.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=K12 / MG1655.
STRAIN=K12 / MG1655.
STRAIN=K12 / MG1655.
BLAILINE-94426617. Pubmed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Characterization of rcsB and rcsC from Escherichia coli 09:K30:H12 and examination of the role of the rcs regulatory system in expression of group I capsular polysaccharides.";
J. Bacteriol. 175:5384-5394(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stout V., Gottesman S.; "ResB and ResC: a two-component regulator of capsule synthesis in Escherichia coli.";
                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBL_TaxID=562;
                                                                          RCSC_ECOLI STANDARD; PRT; 949 AA.
P14776; P76457; P97170; P97202; Q47586;
01-0AN-1990 (Rel. 13, Created)
28-FFB-2003 (Rel. 42, Last sequence update)
15-SFP-2003 (Rel. 42, Last annotation update)
Sensor protein rcsC (EC 2.7.3.-) (Capsular synthesis regulator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-09:K30:H12;
MEDLINE-9374832; PubMed=8366025;
Jayarane-9-, Keenleyside W.J., Maclachlan P.R., Dodgson C.,
Whitfield C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=K12;
MEDLINE=97251358; PubMed=9097040;
                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=K12;
MEDLINE=90130299; PubMed=2404948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Bacteriol. 172:659-669(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                           component C).
RCSC OR B2218.
Escherichia coli.
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between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified anorprofit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R EGOGGNES EALORAZI TERMO3594 ATPDING ATPASE.

R InterPro; IPR003594 ATPDING ATPASE.

R InterPro; IPR003654 Bact_sens_pr_C.

R InterPro; IPR003667; His_Kinas.

R InterPro; IPR001789; Response_reg.

InterPro; IPR001789; Response_reg.

R Pfam; PF00512; HayTesse_c; 1.

R Pfam; PF00512; HayTesse_c; 1.

R PRINTS; PR00344; ECTRISENSOR.

R PRNTS; PR00344; ECTRISENSOR.

R PRNTS; SM00387; HayTesse_c; 1.

R SWART; SM00387; HayTesse_c; 1.

R SWART; SM00391; PAS; 1.

R PROSTITE; PS50110; RESPONSE_REGULATORY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 STTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLIKDKI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.3%; Score 171.5; DB 1; Length 949; llarity 33.9%; Pred. No. 8.6e-07; Conservative 32; Mismatches 37; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
PERIPLASMIC (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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ID FRZE_M
AC P18769
DT 01-NOV
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RESULT 7
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                                                                                                                                                                                                                                                                                                MEDLINE=9107208; Pubmed=2123853; MCGLeary W.R., Zusman D.R.; MCGLeary W.R., Zusman D.R.; MCGLeary W.R., Zusman D.R.; Purification and characterization of the Myxococcus xanthus FrzE protein shows that it has autophosphorylation activity."; J. Bacteriol, 172:6681-668(1990).

-i- FUNCTION: FRZE IS INVOLVED IN A SENSORY TRANSDUCTION PATHWAY THAT CONTROLS THE FREQUENCY AT WHICH CELLS REVERSE THEIR GLIDING DIRECTION: FRZE SEEMS TO BE CAPABLE OF AUTOPHOSPHORYLATING ITSELF ON AN HISTIDINE RESIDUE AND TERN TO TRANSFER THAT GROUP TO AN ASPARTATE RESIDUE IN THE C-TERMINAL PART OF THE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESPONSE REGULATORY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
                                                                                                                                                                                           McCleary W.R., Zusman D.R.; "FrzB of Myxococus xanthus is homologous to both Chea and CheY of Salmonella typhimurium"; Proc. Natl. Acad. Sci. U.S.A. 87:5898-5902(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALA/PRO-RICH (POSSIBLE HINGE REGION). 9912BD40991C69E5 CRC64;
                                                                                       Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
Cystobacterineae; Myxococcaceae; Myxococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transferase; Kinase; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -: SIMILARITY: Contains 1 chew-like domain.
-: SIMILARITY: Contains 1 histidine kinase domain.
-: SIMILARITY: Contains 1 hPT domain.
-: SIMILARITY: Contains 1 response regulatory domain.
01-NOV-1990 (Rel. 16, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Gliding motility regulatory protein (EC 2.7.3.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HISTIDINE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HPT; 1.
RESPONSE_REGULATORY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A35966; A35966.

BSSP; O56310, 1830.

InterPro; IPR001594; ATPbind_ATPase.

InterPro; IPR001594; CheW.

InterPro; IPR001596; CheW.

InterPro; IPR0015467; His_Kinase.

InterPro; IPR001789; Response_reg.

Fam; PF01564; CheW; 1.

Pfam; PF01564; CheW; 1.

Pfam; PF01674; Hpt; 1.

Pfam; PF01677; Hpt; 1.

Pfam; PF01677; Hpt; 1.

Pfam; PF01677; Response_reg; 1.

PRNNTS; PR00344; BCTRLSENSOR.

PRODAGON; PD000039; Response_reg; 1.
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                                                                                                                                                                              MEDLINE-90332690; PubMed-2165608;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS50851; CHEW; 1.
PS50109; HIS_KIN; 1.
PS50894: HPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M35192; AAA25396.1; -.
                                                                                                                                                                                                                                                                                    PHOSPHORYLATION OF HIS-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00260; CheW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sensory transduction;
DOMAIN 1 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00073; HPT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SM00448; REC
                                                                         Myxococcus xanthus.
                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50851;
PROSITE; PS50109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50894;
PROSITE; PS50110;
                                                                                                                           NCBI_TaxID=34;
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DOMAIN
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DB 1; Length 777;

23.1%; Score 156.5;

Query Match

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                                                                                                        657 KRLRVLLVDDSPIARATEGALVKALGHSVEEAQDGEEAYV--KVQNNTYDLILTDVQMPK 714
                                                               14 KKLNVLIVDDDPLNLITHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPE 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=44042864; PubMed~8226633;
Brown J.L., North S., Bussey H.;
"SKN7, a yeast multicopy suppressor of a mutation affecting cell wall
beta-glucan assembly, encodes a product with domains homologous to
prokaryotic two-component regulators and to heat shock transcription
factors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PATRWAY.";
EMBO J. 13:5166-5194(1994).
EMBO J. 13:5166-5194(1994).
INVOLVED IN OXIDATIVE STRESS. TRANSCRIPTION FACTOR THAT
MAY FOUNCTION: IN A TWO-COMPONENT SIGNAL TRANSDUCTION PARHWAY THAT
ACTS IN PARALLEL WITH THE PKCI CASCADE TO REGULATE GROWTH AT THE
CELL SURFACE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=2288C / AB972;
STRAIN=24378003; bubmed=8091229;
SIRDINE-54378003; bubmed=8091229;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
Nhan M., Rifkin L., Riles L., St Perer H., Trevaskis E., Vaughan K.,
Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                   5; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brown J.L., Bussey H., Stewart R.C.; "Yeast Skn?p functions in a eukaryotic two-component regulatory
                                                                                                                                                   74 RDGVSTTKKLREMEVKSMI--VGVTSLADNEEERRAFMEAGLNHCLAK 119
                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Krems B., Charizanis C., Entian K.-D.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: Contains 1 response regulatory domain.
                                                                                                                                                                                                                                                                                                       SKN7_YEAST STANDARD; PRT; 622 AA. P3869; P39747; Created)
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative transcription factor SKN7 (PoS9 protein).
SKN7 OR POS9 OR BRYI OR YHR206W
ilarity 35.2%; Pred. No. 1,2e-05;
Conservative 27; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteriol. 175:6908-6915(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 265:2077-2082(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-95045411; PubMed-7957083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION, AND MUTAGENESIS.
Best Local Similarity
Matches 38; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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DOMAIN
TRANSMEM
DOMAIN
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"Genome
69 KEMPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKI-- 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 IKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVII---HRDGGSSFDLILMD
                                                               PIR; A49344; A49344.

REASP, P20121; 2HTS.

REASP, P201212; 2HTS.

REASP, SOUTHERS, Concleus; IDA.

SGD; SOUO01563; Erva-component response regulator activity; IDA.

GO; GO:0000563; Erva-component response regulator activity; IDA.

GO; GO:0000156; Frva-component response regulator activity; IDA.

GO; GO:0000156; Frva-component response regulator activity; IDA.

RO; GO:0000156; Frva-component response regulator activity; IDA.

GO; GO:0000156; Frva-component response regulator activity; IDA.

RO; GO:0000156; Frva-component response regulator activity; IDA.

RO; GO:0000156; Frva-component response regulator; IRRO01789; Response_reg;

REASP, RESPONSE_REGULATOR; IDA.

RART; SMO04415; HSF_DNA_bind; I.

RART; SMO04415; HSF_DNA_bind; I.

REASPONSE_REGULATOR; I.

RESPONSE_REGULATOR; I.

REASPONSE_REGULATORY; I.

RART; SMO04415; HSF_DNAIN; I.

REASPONSE_REGULATORY; I.

RAPEDIATE; PSSO110; RESPONSE_REGULATORY; I.

RAPEDIATE; PSSO110; RESPONSE_REGULATORY; I.

RAPEDIATE; PSSO110; RESPONSE_REGULATORY; I.

RAPEDIATE; PSSO110; RESPONSE_REGULATORY; I.

RAPEDIATE; RAPEDIATE; PSSONSE_REGULATORY; I.

RAPEDIATE; PSSO110; RESPONSE_REGULATORY; I.

RAPEDIATE; PSSO110; RESPONSE_REGULATORY; I.

RAPEDIATE; RAPEDIATE; PSSONSE_REGULATORY; I.

RAPEDIATE; PSSO110; RESPONSE_REGULATORY; I.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (1) SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. MEDLINE-21074935, PubMed-11206551; MEDLINE-21074935, PubMed-11206551; MEDLINE-21074935, PubMed-11206551; Medline-21074935, PubMed-111, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Kilnk S., Boutin A., Shao Y., Miller L., Acotheck E.J., Davis N.W., Lim A., Dimalante E.T., Pottamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Melch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae, Escherichia.
NCBL_TaxID=83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Aerobic respiration control sensor protein arcB (EC 2.7.3.-).
ARCB OR Z4574 OR ECS4089.
Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.1%; Score 150; DB 1; Length 622;
28.1%; Pred. No. 3.3e-05;
Live 32; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESPONSE REGULATORY.
PHOSPHORYLATION (PROBABLE).
D-N: DIMINISHED ACTIVITY.
4C732FD66E326742 CRC64;
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427 427 D-
427 427 D-
622 AA; 69202 MW;
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                  EMBL; U000485; AAC48911.1; -. EMBL; X83031; CAA58143.1; -. EMBL; U00029; AAB69734.1; -.
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Best Local Similarity 28.1
Matches 38; Conservative
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P58363;
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MUTAGEN
MUTAGEN
SEQUENCE
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DOMAIN
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                                                                                      SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SETAIN=0157:H7 / RIMD 0509952;

MEDLINE=2115623; PubMed=11258796;

Hayshi T., Makino K., Chnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino E., Nakayama K., Murata T., Tanaka M., Tobe T., A. Hayashi T., Hattori M., Shinagawa H.; Tobe T., A. Kuhara S., Shiba T., Hattori M., Shinagawa H.; Scherichia coli Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 811-22(2001).

C. I- FUNCTION: Member of the two-component regulatory system arcB/arcA.

Sensor-regulator protein for anaerobic repression of the arc modulon Activates arcA via a four-step phosphorelay. ArcB can also dephosphorylate arcA by a reverse phosphorelay. ArcB can also dephosphorylate arcA by a reverse phosphorelay involving Historylate.

C. -- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enome sequence of enterohaemorrhagic Escherichia coli O157:H7."; ture 409:529-533(2001).
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PROSITE; PS50109; HFS_KIN; 1.
PROSITE; PS5084; HPT; 1.
PROSITE; PS50113; PAC; 1.
PROSITE; PS50112; PAS; 1.
PROSITE; PS50110; PAS; 1.
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PIR: D85985: D85985: InterPro; IPR003594; ATPbind_ATPase. InterPro; IPR003594; ATPbind_ATPase. InterPro; IPR003504; His_Kinase. InterPro; IPR0005467; His_Kinase. InterPro; IPR000704; PAS_domain. InterPro; IPR000104; PAS_domain. InterPro; IPR000199; PAS_domain. InterPro; IPR00199; Response_reg; Pfam; PF00312; HiskA; 1. Pfam; PF00312; HiskA; 1. Pfam; PF00312; HiskA; 1. Pfam; PR00072; response_reg; 1. Pr00072; response_reg; 1. SMART; SM00389; HiskA; 1. SMART; SM00389; HiskA; 1. SMART; SM0091; PAS; 1. SMART; SM0091; PAS; 1.
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134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
MEDLINE=2272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Zhang X., Zhang Y., Zhang J., Kang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
                                                                                                                                                                                                                     16 INVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERD
                                                                                                                                                                                                                                                                                   76 GVSTTKKLREMEVKSMIVGVTSLADNE-EERRAFMEAGLNHCLAKPLTKDKIIPLINQLM
                                                                         PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
C8AE004E007F9D30 CRC64;
                                                                                                                                                                                        Gaps
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SEQUENCE FROM N.A.
SPECIES-E coli; STRAIN-K12 / MG1655;
MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riathy M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBL_TaxID=562, 623;
                                                                                                                                                     22.1%; Score 149.5; DB 1; Length 778; 25.6%; Pred. No. 4.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1991 (Rel. 19, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Acrobic respiration control sensor protein arcB (EC 2.7.3.-).
ARCB OR B3210 OR SF3250.
Escherichia coli, and
Shigella flexneri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete genome sequence of Escherichia coll K-12.", Science 277:1453-1474(1997).
                                                                                                                                                                                      Indels
                                                                                                                                                                                      47;
                               HISTIDINE KINASE.
RESPONSE REGULATORY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          778 AA
                                                                                                                                                                                      40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                            88010 MW;
                                                                                                                                                                                        Conservative
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153
226
289
527
678
292
576
717
718 AA;
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P22763:
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Best Local S
Matches 31
                                                DOMAIN
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MOD_RES
MOD_RES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.57.A resolution.";
Acta Crystalludor. D 55:1842-1849(1999).
-!- FUNCTION: Member of the two-component requiatory system arcB/arcA.
-!- FUNCTION: Member of the two-component requiatory system arcB/arcA.
Sensor-requiator protein for anaerobic repression of the arc
modulon. Activates arcA via a four-step phosphorelay. ArcB can
also dephosphorylate arcA by a reverse phosphorelay involving His-
717 and Asp-576.
-!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                 SPECIES=E.coli, STRAIN=M15;
MEDLINE-99047671; PubMed-9830034;
Georgellis D., Kwon O., De Whif P., Lin E.C.C.;
"Signal decay through a reverse phosphorelay in the arc two-component signal transduction system.";
J. Biol. Chem. 273:32864-32869(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kato M., Mizuno T., Hakoshima T.;
"Crystallization of a complex between a novel C-terminal transmitter, HPt domain. of the anaeroic sensor kinase ArcB and the chemotaxis response regulator Chey."
Acta Crystallogr. D 54:140-142(1998).
                                                                                                                                                                                                                                                                                                                                                                                     by the arc two-component system of Escherichia coli."; J. Bacteriol. 182:3858-3862(2000).
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MEDLINE-20003135; PubMed=10531481;
Atto M., Mizuno T., Shimizu T., Hakoshima T.;
"Refined structure of the histidine-containing-phosphotransfer (HPt)
domain of the anaerobic sensor kinase ArcB from Escherichia coli at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.06 ANGSTROMS) OF 660-778.
SPECIES=E.coli;
MEDLINE=97207018; PubMed=9054511;
MIZUNO T., Shimizu T., Hakoshima T.;
"Insights into multistep phosphorelay from the crystal structure of the C-terminal HPt domain of ArcB.";
cell 88:717-723(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- SIMILARITY: Contains 1 histidine kinase domain.
-:- SIMILARITY: Contains 1 HPT domain.
-:- SIMILARITY: Contains 1 PAS-(ERP.ARNT-SIM) dimerization domain.
-:- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
-:- SIMILARITY: Contains 1 response regulatory domain.
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SPECIES=E.coli; STRAIN=M15;
MEDLINE=97431492; PubMed=9286997;
Georgellis D., Lynch A.S., Lin E.C.C.;
"In vitro phosphorylation study of the arc two-component signal transduction system of Escherichia coli.";
J. Bacteriol. 179:5429-5435(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 659-776 IN COMPLEX
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                                                                                                                                                                                                                                                                                                                   HIS-717
                                                                                                                                                                                                                                                                                                                                                                                   Kwon O., Georgellis D., Lin E.C.C.;
"Phosphorelay as the sole physiological
                                                                                                                                                                                                                                                                                                                                          SPECIES=E.coli; STRAIN=K12 / MC4100;
MEDLINE=20309722; PubMed=10851007;
                                                                                                                                                                                                                                                                                                                      MUTAGENESIS OF HIS-292; ASP-576 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES=E.coli;
MEDLINE=98437504; PubMed=9761838;
                                                                                                                                                    CHARACTERIZATION.
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SLN1_YEAST
P39928;
                 SLN1_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sensory transduction; Transferase; Kinase; Phosphorylation; Transmembrane; Inner membrane; Transcription regulation; 3D-structure; Complete proteome.

Complete proteome. 25 CYTOPLASMIC (POTENTIAL).
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PHOSPHORYLATION (PROBABLE).
PHOSPHORYLATION (PROBABLE).
H->Q: LOSS OF ACTIVITY.
D->A: LOSS OF ACTIVITY.
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DD61EA6ECF95AD30 CRC64;
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PERIPLASMIC (POTENTIAL).
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RESPONSE REGULATORY.
                                                                                                                                                                                       InterPro; IPR003594; ATDPING ATPASE.
InterPro; IPR003594; Bact_sens_pr_C.
InterPro; IPR003561; His_KinA.
InterPro; IPR003561; His_KinA.
InterPro; IPR002570; Hpt_xinase.
InterPro; IPR00070; PAS_assoc_C.
InterPro; IPR00070; PAS_assoc_C.
InterPro; IPR001789; Response_reg.
Pfam; PF00512; HisKA; I.
Pfam; PF00989; PAS; 1.
Pfam; PF00989; PAS; 1.
Pfam; PF00989; PAS; 1.
ProDom; PD000039; Response_reg; 1.
PRNWTS; ER00948; HisKA; I.
SWART; SW00091; PAS; 1.
SWART; SW00091; PAS; 1.
SWART; SW00091; PAS; 1.
SWART; SW00091; PAS; 1.
PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS501109; HS_KIN; 1.
PROSITE; PS501101; PAS; 1.
PROSITE; PS50111; PAS; 1.
PROSITE; PS50110; PAS; 1.
PROSITE; PSS0110; PAS; 1.
PASPONSE PASPONSE PROSIDERE PASPONSE PASP
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X53315; CAA37397.1; -. U18997; AAA58012.1; -. AE000400; AAC76242.1; - AE015336; AAN44715.1; -
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                                                                                             PDB: 140B: 18-MAR-98.
PDB: 2A0B: 17-JUN-98.
PDB: 18DJ: 11-MAY-99.
PDB: 1FR0; 31-DEC-02.
ECOGENE: EG10062; arcB
                                                                            PIR; D65112; RGECAR.
PDB; 1A0B; 18-MAR-98
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778 AA;
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PSINALINE STRANDARY STRANDARY PREF, 1220 AA.

PSINALINE STRANDARY STRANDARY PREF, 1220 AA.

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712 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESPONSE REGULATORY.
PHOSPHORYLATION (ATTO-) (PROBABLE).
PHOSPHORYLATION (ATTO-) (PROBABLE).
N-LINKED (GLCNAC...) (POTENTIAL).
H->0: INACTIVE.
G->N: INACTIVE.
D->N: INACTIVE.
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SEQUENCE FROM N.A., AND MUTAGENESIS.
MEDILNE-94239498; PubMed-8183345;
Maeda T., Wurgler-Wurphy S.M., Saito H.;
Maccomponent system that regulates an osmosensing MAP kinase
cascade in yeast.";
Nature 369:242-245(1994).
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomyceteles;
Saccharomyceteles; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 1220;
                                                                                                                                                                                                                               PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50110; RESPONSE_REGULATORY; 1.
Sensory transduction; Transferase; Kinase; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134434 MW; 45FFE24A8165486B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.4%; Score 145; DB 1; 29.0%; Pred. No. 0.00018; tive 40; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSK1_YEAST STANDARD; PRT; 712 AA. 007084; Q07909; 01-NOV-1997 (Rel. 35, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) 050molarity two-component system protein SSK1. SSK1 OR YLR006C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HISTIDINE KINASE
Pfam; PF02518; HATPASS_C; 1.
Pfam; PF00512; HiskR; 1.
Pfam; PF00072; response_reg; 1.
Probom; PR00344; BCTRLERNSOR.
Probom; PD000039; Response_reg; 1.
SMART; SM00387; HATPASS_C; 1.
SMART; SM00388; HiskR; 1.
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MEDLINE=97313267; PubMed=9169871;
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Best Local Similarity
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TRANSMEM
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MOD_RES
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CARBOHYD
CARBOHYD
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MUTAGEN
SEQUENCE
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this SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 EMPERDGVSTTKKLREMEVKS------101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 EKIKKKLNVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDK
Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W., Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A., Entian K.-D., Floeth M., Goffeau A., Hebling U., Heumann K., Louis E.J., Messenguy F., Mellen F., Kleine K., Koetter P., Mueller Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M., Worlterle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Scherens B., Scholler P., Schwarz S., Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P., Vierendeels F., Voet M., Volckaert G., Voss H., Wamburt R., Wedler E., Wedler H., Zimmermann F.K., Zollner A., Hani J., Hohelsel J.D., The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.", Nature 387:87-90(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                             "NOTION: FORMS PART OF A TWO-COMPONENT REGULATORY SYSTEM
-!- FUNCTION: FORMS PART OF A TWO-COMPONENT REGULATORY SYSTEM
SLN1/SSK1 ACTIVATED BY CHANGES IN THE OSNOLARITY OF THE
SETRARGELLUARE BUYIRONBENT. THIS SYSTEM CONTROLS THE SK2/SSK22->
BESTRARGELLUARE BUYIRONBENT. THIS SYSTEM CONTROLS THE SK2/SSK22->
BNSC->-HOG1 PATHWAY. THE UNPHOSPHORYLATED FORM OF SSK1 ACTIVATES
SK2 AND SSK22, TWO MAPKKS THAT FURTHER STIMULATE THE PBS2-HOG1
MAPK ACSCADE. IN LOW-OSNOLARITY MEDIA, IS INHIBITED THROUGH THE
PHOSPHORYLATION BY SIN.
-!- SUBCELLULAR LOCATION: CYCOPLSMIC (POCENIAL).
-!- SUBCELLULAR LOCATION: CYCOPLSMIC (POCENIAL).
-!- SUBCELLULAR LOCATION: CYCOPLSMIC (POCENIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION (PROBABLE).
D-N: ACTIVATES.
P -> S (IN REF. 1).
33B2DBB4FCF2528A CRC64;
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01-FEB-1996 (Rel. 33, Last sequence update)
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Matches 39; Conservative
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554
181
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226 AA
                                                                                                                         33; Mismatches
                                                                                      20.9%; Score 142; 27.6%; Pred. No. 0
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284 PF
707 PF
853 PF
99195 MW;
                                                                                        Query Match
Best Local Similarity 27.69
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                           124 DKIIPLI 130
                                                                                                                                                                                                                                                                                                                                  284
707
853
907 AA;
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MOD_RES
MOD_RES
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
DCTR_BACSU
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     FFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                         regulators.";
J. Bacteriol. 174:3011-3020(1992).
J. Bacteriol. FORMS PART OF A TWO-COMPONENT REGULATORY SYSTEM
-!- FUNCTION: FORMS PART OF A TWO-COMPONENT REGULATORY SYSTEM
GACA/GACS(LENA). MAY BE INVOLVED IN LESION FORMATION, SWARMING AND
IN THE PRODUCTION OF EXTRACELLULAR PROTEASE, SYRINGOMYCIN AND N-
ACYL-L-HOMOSERINE LACTONE (ACYL-HSL). REQUIRED FOR PATHOGENICITY
                                                                                                                                                                                                                                                                                                                                                                                                  -. FILLOWING Activation requires a sequential transfer of a phosphate group from a H1s in the primary transmitter domain, to an Asp in the receiver domain and to a H1s in the secondary transmitter domain (By similarity).
-: SIMILARITY: Contains 1 HAMP domain.
-: SIMILARITY: Contains 1 H5tidine kinase domain.
-: SIMILARITY: Contains 1 HPT domain.
-: SIMILARITY: Contains 1 HPT domain.
                                                                                                                                                                                                   "The lemA gene required for pathogenicity of Pseudomonas syringae pv. syringae on bean is a member of a family of two-component
                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                           Pseudomonas syringae (pv. syringae).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50894; HPT; 1.
PROSITE; PS50110; RESPONSE_REGULATORY; 1.
Sensory transduction; Transferase; Kinase; Phosphorylation; Transmembrane; Inner membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
POTENTIAL.
HAMP.
HISTIDINE KINASE.
RESPONSE REGULATORY.
HPT.
           Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR004589; Back_SenS_Dr_C.
InterPro; IPR004560; HAMP.
InterPro; IPR003660; HAMP.
InterPro; IPR003660; His_kina.
InterPro; IPR003667; His_kinase.
InterPro; IPR001789; Response_reg.
Fram; PF00572; HAMP; 1.
Pfam; PF00512; HSKA; 1.
Pfam; PF00512; HSKA; 1.
Pfam; PF00534; HAMP; 1.
SMART; SM00304; HAMP; 1.
SMART; SM00387; HAMP; 1.
SMART; SM00387; HAMP; 1.
SMART; SM0073; HPT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro, IPR003594; ATPbind_ATPase.
Interpro, IPR004358; Bact_sens_pr_C.
                       Sensor protein gacs (EC 2,7.3.-). GACS OR LEMA.
                                                                                                                                                                    MEDLINE=92234961; PubMed=1314807;
Hrabak E.M., Willis D.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50885; HAMP; 1.
PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50894; HPT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M80477; AAA25877.1; -.
HSSP; P06143; 1UDR.
                                                                                                                                                  SEQUENCE FROM N.A.
           28-FEB-2003 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                          (Probable).
                                                                                                                  NCBI_TaxID=321;
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TRANSMEM
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MEDLING-98044033; PubMed-938437;
RA MINET: V. Ogasawara N., Moszer I., Albertini A., Borchert S.,
Azevedo V., Bertero M.G., Bessaeres P., Bolothn A., Borchert S.,
RA Borriss R., Beureier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Buuschic C., Caplano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.P., Cummings N.J., Daniel R.A.,
RA brian R.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fabret C., Ferrari E., Foulger D.,
RA Gilseppl G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Eolsappel S., Hosoño S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Joris B., Levine A., Lardinois S., Lauber J., Lazarevic V.,
RA Kunita K., Lapidus A., Lardinois S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Miluno M., Moseil D., Nakai S., Noback M.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Perscott A.M.,
RA Presecon B., Pujic P., Purnelle B., Rapoport G., Rey M., Raynolds S.,
RA Sekvaka A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Fieger M., Tamakoshi A., Tarakashi H., Takamaru K.,
RA Tosaco V., Uchiyama S., Vandenbol M., Vannier P., Viari A., Wannbutt R., Wannbutt R., Wannbutt R., Wannbutt R., Wannbutt R., Wannbutt R., Yasumoto M., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 KEMPERDGVSTTKKLREMEVKS-----MIVGVTSLADNEEERRAFMEAGLNHCLAKPLTK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 VLIVDDDPLNLITHEKIIKAIGGISQTANNGEEAVIIHRDGG-----SSFDLILMD
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Assahara N.; Nakai S., Lee S., Sadaie Y., Ogasawara N.; Assahara kbp sequence of the region between 35 and 47 degree of the Bacillus subtilis genome."; Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                   Score 142; DB 1; Length 907; Pred. No. 0.00023;
                                                                                                                                                                                                                                                                                                               33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus
                                                                                                                                     5B9F4663DAF3492C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P96602; P94503;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Probable C4-dicarboxylate response regulator dctR.
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Probable C4-dicarboxylate response regulator dctR.
DCTR OR BH2751.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chemotaxis protein cher homolog CHEY OR CHEB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AP001516; BAB06470.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 29.4
Matches 35; Conservative
                                               Bacteria; Firmicutes;
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=168 / OI1085;
                                      Bacillus halodurans.
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DNA_BIND
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 KKKLNVLIVDDDPLNLIHEKIIKAIGGIS--QTANNGEEAVIIHRDGGSSFDLILMDKE 70
                                                                                                                                                                                                                                                             Asai K., Baik S.-H., Kasahara Y., Moriya S., Ogasawara N.;
"Regulation of the transport system for C4-dicarboxylic acids in
Bacillus subtilis."
Microbiology 146:263-271(2000).
-i. FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM DCTS/DCTR.
ESSENTIAL FOR EXPRESSION OF DCTP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71 MPERDGVSTIKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 MPKKDGIKTLQEIRKQKLEVDVI-VVSAAKDKETISIMLQNGAVDYILKFFKLERM 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
       complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.7%; Score 140.5; DB 1; Length 226; 25.9%; Pred. No. 6.7e-05; Live 39; Mismatches 42; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHOSPHORYLATION (BY SIMILARITY).
H-T-H MOTIE (POTENTIAL).
T IN REF. 3).
018115B14E9EF470 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PSS0110; RESPONSE_REGULATORY; 1.
Sensory transduction; Transcription regulation; DNA-binding; Activator; Phosphorylation; Complete proteome.
DOMAIN 123
                                                                                                                     Morel-Deville F., Ehrlich S.D., Morel P.; "Identification by PCR of genes encoding multiple response requiators.";
                                                                                                                                                                                                                                                                                                                                                               -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-1- PTM: PHOSPHORYLATED BY DCTS (PROBABLE).
-1- SIMILARITY: Contains 1 response regulatory domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AB001488: BAL19283.1;
EMBL, 0293106; CAB12253.1;
EMBL, 082580; AB41751.1;
PIR, B69771; B69771.
HSSP, Q56312; ITMY
Subtilist: B612074; dctR.
InterPro; IPR01789, Response_reg,
Pfam, PF00072, response_reg; 1.
PIRSF, PTSEF006171; RR_Catrat_malat; 1.
Probom; PD000039; REC; 1.
                                                                                                                                                                                                                                  MEDLINE-20170658; PubMed-10708364; Asai K., Baik S.-H., Kacahara
                                                                                                              MEDLINE-97311990; PubMed-9168601;
                                                                                                                                                                              Microbiology 143:1513-1520(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 206 H
24 24 F
226 AA; 25539 MW;
                                                                             SEQUENCE OF 14-101 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                          Nature 390:249-256(1997).
                                                                                                                                                                                                                   FUNCTION, AND GENE NAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (
16-OCT-2001 (
28-FEB-2003 (
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Q9K998;
                                                                                                                                                                   regulators.
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DCTR_BACHD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 LNVLIVDDDPLNLIIHEKIIKAIGG--ISQTANNGEEAVIIHRDGGSSFDLILMDKEMPE 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74 RDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLINQ 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
Horikoshi K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     υ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 59 PHOSPHORYLATION (BY SIMILARITY).
183 209 H-T-H MOTIF (POTENTIAL).
230 AA; 26376 MW; 06FD65F46FC57D40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE: PS50110; RESPONSE REGULATORY: 1. Sensory transduction; Transcription regulation; DNA-binding; Activator; Phosphorylation; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus. NCBI_TaxID=1423;
Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESPONSE REGULATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.7%; Score 140.5; DB 1
29.4%; Pred. No. 6.9e-05;
Live 32; Mismatches 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHEY_BACSU STANDARD; FRT; 119 AA. 124072; P37583; 01-M271995 (Rel. 21, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; G83993; G83993.
HSSP; P10957; IRNL.
InterPro; IPR001789; Response_reg.
Pfam; PF00072; response_reg; 1.
Probom; PD000039; Response_reg; 1.
SMART; SM00448; REC; 1.
                                                                               SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
MEDLINE-20512582; PubMed=11058132;
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64

DAPPE

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MEDLINE=91286247; PubMed=1905718;

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                                                                                                                                                                                                                          RA Kunstr. Ogasawara N., Moszer I., Albertini A.M., Alloni G., Raunstr. Ogasawara N., Moszer I., Albertini A.M., Borchert S., Ravedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Ravedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Raville S., Buuschi C.V., Caldwell B., Capuano V., Catter N.M., R. Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Catter N.M., Chois S.K., Codani J.J., Connetron I.F., Cummings N.J., Daniel R.A., R. Entlich S.D., Emmerson P.T., R. Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Faritz C., Fujita M., Fujita Y., Fune S., Galizzi A., Galleron N., R. Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A., R. Hibbert H., Holsappel S., Hasono S., Hullo M.F., Itaya M., Jones L., R. Hibbert H., Holsappel S., Hasono S., Hullo M.F., Itaya M., Jones L., R. Hibbert H., Rolsappel S., Hasono S., Hullo M.F., Itaya M., Jones L., R. Horis B., Karamata D., Kasahara Y., Klauter Blanchard M., Klein C., R. Hedina N., Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C., Redina M., Levine A., Liu H., Masuda S., Mauel C., Medigue C., Re Media N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Rapero V., Pohl T. M., Pogawa K., Ogiwara A., Oudega B., Park S.H. Rapero V., Pohl T. M., Pogawa K., Ogiwara A., Oudega B., Park S.H. Rapero V., Pohl T. M., Pottetelle D., Porwollik S., Prescott A.M., Rieger M., Rivolta C., Rocha E., Roche M., Sadaie Y., Rakeuchi M., Tamakoshi H., Tamakoshi H., Tamakoshi A., Tanaka T., Takahashi H., Tamakoshi A., Tanaka T., Takahashi H., Wambutt R., Wandler E., W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93078625; PubMed=1447979;
Bischoff D.S., Ordal G.W.;
"Identification and characterization of Flix, a novel component of
the Bacillus subtilis flagellar switch complex.";
Mol. Microbiol. 6:2715-2723(1992).
               Bischoff D.S., Ordal G.W.; "Sequence and characterization of Bacillus subtilis CheB, a homolog of Escherichia coli CheY, and its role in a different mechanism of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-92283757; PubMed=1597417;
Bischoff D.S., Weinreich M.D., Ordal G.W.;
"Nucleotide sequences of Bacillus subtilis flagellar biosynthetic
genes filt and filt and identification of a novel flagellar gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-12.
SEQUENCE OF 1-12.
MEDLINE-96345629; PubMed-8755892;
Graumann P., Schroeder K., Schmid R., Marahiel M.A.;
Graumann P., Schroeder K., Schmid R., Marahiel M.A.;
"Cold shock stress-induced proteins in Bacillus subtilis.";
J. Bacteriol. 178:4611-4619(1996).
J. Bacteriol. 178:4611-4619(1996).
J. FUNCTION: HAS A CENTRAL CONTROLLING ROLE IN CHEMOTAXIS.
IT IS HOMOLOGOUS TO THE CHEY PROTEIN OF OTHER BACTERIA,
THOOGHT TO FUNCTION IN A DIFFERENT MANNER.
-1. SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                     Biol. Chem. 266:12301-12305(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Bacteriol. 174:4017-4025(1992)
                                                                                                                                                                                                            MEDLINE-98044033; PubMed-9384377;
Kunst F., Ogasawara N., Moszer T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 95-119 FROM N.A. STRAIN-168 / OI1085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 390:249-256(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=168 / OI1085;
                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              18 VLIVDDDP-LNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLIIMDKEMPERDG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 VSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLINQLMD 135
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62 ITALKEIKQIDAQARIIMCSAMGQSMVIDA-IQAGAKDFIVKPFQADRVLEAINKTLN 119
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1 118 RESPONSE REGULATORY.
53 53 PHOSPHORYLATION (BY SIMILARITY).
119 AA; 13178 MW; F3BCA0F02CAB7531 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 19.8%; Score 134; DB 1; Length 119; 26.9%; Pred. No. 0.00012;
                                                                                                                                                                                                                                                                                                                                                                                                                   47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: August 14, 2003, 16:47:19
Job time : 24 secs
                                                                                           EMBL; M59781; AAA22311.1; --
EMBL; 299112; CAB13506.1; --
EMBL; M86738; AAA22450.1; --
EMBL; M37005; AAA22451.1; --
PIR; A40874; A40874; A40874; Subtilist; B610258; Chey,
Interpro: IPR001789; Response_reg;
Pfam; PF00072; response_reg; 1.
ProDom; PD000039; Response_reg; 1.
SMART; SM00448; REC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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nes 32; Conserv
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SEQUENCE
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Matches
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

August 14, 2003, 16:46:47; Search time 95 Seconds (without alignments) 369.423 Million cell updates/sec Run on:

Title: US-09-646-679-15
Perfect score: 678
Sequence: 1 MATKSWGDIEKIKKKLNVLI.....LAKPLTKDKIIPLINQLMDA 136

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

830525 seqs, 258052604 residues Searched:

830525 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

sp_organelle:*
sp_bhage:*
sp_plant:*
sp_rodent:*
sp_virus:*
sp_virus:*
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sp_virus:*
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sp_virus:*
sp_virus:*
sp_rodent:* SPTREMBL_23:*

1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_inwan:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	& Query Match	Query Match Length DB	DB	H 1	Description
⊣ (678	100.0	136	10	082445	082445 brassica na
7	238	4.6	147	2	CYM814	Q9m8y4 arabidopsis
m	181	26.7	1969	'n	015763	015763 dictyosteli
4	179.5	26.5	820	16	Q8EZ63	Q8ez63 leptospira
S	178.5	26.3	1197	16	Q8CVU5	Q8cvu5 escherichia
φ	174	25.7	394	16	Q9A3P0	Q9a3p0 caulobacter
7	173.5	25.6	949	16	Q8FFP9	Q8ffp9 escherichia
œ	173	25.5	417	N	Q9RLC7	Q9rlc7 pseudomonas
σ	171.5	25.3	933	16	Q8XE39	Q8xe39 escherichia
10	171.5	25,3	957	16	Q8ZGR4	Q8zqr4 yersinia pe
11	171	25.2	927	7	Q9ANYO	Q9anyO vibrio fisc
12	170	25.1	769	16	Q8PQ37	Q8pq37 xanthomonas
13	167.5	24.7	1364	16	OSPJN8	Q8pin8 xanthomonas
14	166.5	24.6	507	7	085663	085663 proteus mir
15	163.5	24.1	1364	16	Q8P883	Q8p883 xanthomonas
16	162.5	24.0	642	16	09A3L2	09a312 caulobacter

Ogge96 emericella Ogge65 xanthomonas Oggu0 dicryosteli Ogg555 dicryosteli Ogg555 dicryosteli Ogg556 vibrio vuln Ogg381 archaeoglob Ogkr16 vibrio vuln Ogg87W3 andbaena sp Ognv2 beurospora Ogac40 caulobacter Ogac40 vibrio chol Ogac42 anthomonas Ogac42 caulobacter Ogac42 shewanella Ogac42 shewanella	
09P896 6 08P869 6 08P062 6 09BD62 6 09BD16 6 08BD16 6 08BP16 6 08BP16 6 08BP16 6 08BP16 6 08BP16 6 09BP16 6 09BP17 7 08BP17 7 08BP17 6 09AF17 6 09AF17 6 09AF17 6 09AF17 6 09AF17 6 09AF17 6 08BP17	•
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ALIGNMENTS

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					Biassica napus (nape). Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;				Roberts J.A.;	"A mRNA encoding a response regulator protein from Brassica napus									136;		, 0	MATKSMGDIEKIKKKLNVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGS	MATKSMGDIEKIKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGS	TEAGLN	
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		te)	date)		phyta	core	.ca.			. M.	from P		the EMBL/GenBank/DDBJ databases						'5 CRC64;			0; I	IGGISC	IGGIS	LADNE	LADNE
:	AA.	ed) sequence update)	annotation update)		Embryc	dons;	Brassi			Taylor V.M.,	otein		/DDBJ						luction. DA99B768FAB3CFF5	DB 1	Pred. No. 4.7e-52;	es	EKLIKA	EKIIKA	IVGVTS	IVGVIS
	136	d) equenc	nnotat		hyta;	cotyle	ceae;			S., Ta	tor pr	نا	enBank					ORY; 1	ion. 9B768F	678	NO.	0; Mismatches	LNLIIH	LNLIH	MEVKSM	MEVKSM
;	PRT;	Created Last sed			reptop	endi	ssica			Whitelaw C.A., Paul W., Jenkins E.S.,	regula	up-regulated during pod development.";	SMBL/G	red.		eg; 1.		PROSITE; PS50110; RESPONSE_REGULATORY;	Phosphorylation; Sensory transduction. SEQUENCE 136 AA; 15055 MW; DA99B76); Mi	TADDDE	TVDDDP	PKKLRE	KKLRE
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	PRELI	(Trem	(Trem	Response regulator protein.	iridil	a, Mad	Bras	(20)	SEQUENCE FROM N.A.	1., Pa	ding	duri	Submitted (APR-1998) to the EMPenbit apple 1999 $^{\circ}$	Interpro: IPR001789: Response req.	Pfam; PF00072; response_reg; 1.	ProDom; PD000039; Response_reg; 1	SMART; SM00448; REC; 1.	0110;	ion; 36 AA		Similarity	Conservative	KSMGD	KSMGD	LILMD	LILMD
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SUI 244		0 10 10		A G						_			RL GG						KW PO	Ouer	Best	Matches	٥y	qq	٥y	Db
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SEQUENCE FROM N.A.
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Gaps
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SEQUENCE FROM N.A.

STRAIN=CV. Columbia;

Lin X. Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,

Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,

Ronning C.M., Koo H., Fujii C.Y., C., Fraser C.M.;

"Arabidopsis thaliana chromosome III BAC TGK12 genomic sequence.";

Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Feldmann K.A., Flavell R.B., White O., Salzberg S.L.: "Full-length messenger RNA sequences greatly improve genome annotation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 538; DB 10; Length 142; Pred. No. 9.8e-40;
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Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
Feldmann K.;
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79.4%; Score 538; DB 10; Length 14
Best Local Similarity 78.9%; Pred. No. 9.86-40;
Matches 112; Conservative 8; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative response regulator protein (receiver component).
16K12.10.
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Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AC016829; AAF26786.1; --
EMBL; AY086538; AAM62059.1; --
InterPro; IPR001789; Response_reg.
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Probon: P0000139; Response_reg; 1.
PROSITE; PS50110; RESPONSE_REGULATORY; 1.
Phosphory lation; Sensory transduction.
SEQUENCE 142 AA; 15792 MW; 57487135FF2D5238 CRC64;
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015763 (TEMBLEL. 05, Created)
01-JAN-1998 (TEMBLEL. 05, Last sequence update)
                                                                                                                                                                                                                                                                                                                 142 AA.
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                                                    121 LTKDKIIPLINGLMDA 136
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Genome Biol. 0:0-0(2002).
                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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70 EMPERDGVSTTKKLREMEVKSMI-----VGVTSLADNE--EERRAFMEAGLNHCL 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.7%; Score 181; DB 5; Length 1969;
35.8%; Pred. No. 5.1e-07;
ive 29; Mismatches 39; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                A Linda M.J., Singleton C.K.;

B Loc. Biol. 1961.11-183 (1998).

B EMBL; AF024654; AAB11889.1: -

B InterPro: IPR000354; ATPbind_ATPase.

B InterPro: IPR000356; His.KinA.

B InterPro: IPR000367; His.KinA.

B InterPro: IPR00044; PAS.Comain.

B Fam; PF00512; HisRA.;

B Fam; PF00512; HisRA.

B PRINTS; PR00034; Response_reg; 1.

B PRINTS; PR00034; Response_reg; 1.

B PRNRT; SM00038; Response_reg; 1.

B SMART; SM00038; Response_reg; 1.

B SMART; SM00038; Response_reg; 1.

B SMART; SM00031; PAS: 1.

B SMART; SM00048; HisRA.; 1.

B PROSITE; PS50109; HISRA.; 1.

B PROSITE; PS50109; HISRA.; 1.

B PROSITE; PS50109; HISRA.; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leptospira interrogans.
Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
NCBI_TaxID=173;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kinase; Phosphorylation; Sensory transduction.
SEQUENCE 1969 AA; 219025 MW; 8E7A7952AB1BB52B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB011554; AAN$1193.1; -.
Complete protecme.
SEQUENCE #20 AA; 94325 MW; 3DBE99966794E67D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Two-component hybrid sensor and regulator.
LA3996.
                                                                                       ictyostelium discoideum (Slime mold).
Jkaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hybrid histidine kinase DHKB.
                                                                                                                                                                                                                                              STRAIN=KAx3;
MEDLINE=98248997; PubMed=9576830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 AKPL-TKDKIIPLI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 35.8'
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 QLM 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              380 SLL 382
                                                                                                                                                                                                                                                                                                                                                                                                       TIGR; CC3162; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8FFP9
Q8FFP9;
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OBFFP9
g
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                                                                                                                           63 DLILMDKEMPERDGVSTTKKLREMEVKS---MIVGVTSLADNEEERRAFMEAGLNHCLAK 119
                                                                                                                                                                                                                        737 DIILMDIHMPEVDGIEATKWIRSKNQNSEFPIIIALTADA-IESSKEKYISKGMNDCLTK 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 IKKKLNVLIVDDDFLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEM 71
                                                                                                   8 DIEK-----IKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSF 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            955 LPEKLSILIADDHPTNRLLLKRQLNLLGYDVDEATDGVQA--LHKVSMQHYDLLITDVNM
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                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Protecobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBL_TaxID=217992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.3%; Score 178.5; DB 16; Length 1197; 34.4%; Pred. No. 4.6e-07; Live 25; Mismatches 52; Indels 3;
                                                            15;
                   DB 16; Length 820;
                                                          49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transferase; Complete proteome.
SEQUENCE 1197 AA; 134847 MW; 5088214E7F834F06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 12, Last annotation update)
Sensor histidine kinase/response regulator.
CC3162.
Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                                                                                                            01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Sensor protein evgS precursor (EC 2.7.3..).
                 Query Match 26.5%; Score 179.5; DB 1
Best Local Similarity 31.6%; Pred. No. 2.4e+07;
Matches 43; Conservative 29; Mismatches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394 AA.
                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1197 AA
                                                                                                                                                                                                                                                               120 PLTKDKIIPLINQLMD 135
                                                                                                                                                                                                                                                                                                        796 PLD----LPILKSTLD 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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es 42; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli 06.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 QL 133
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Q9A3P0;
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09A3P0
1D 09A3I
DT 01-01
DT 01-01
DT 01-01
ON CC3IS
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                                                                                                                                                                                                                                                                                                                                                            RESULT 5
Q8CVU5
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262 RSAHILIVDDNATURMVAEALCDMFECTSEQAVDGVEAVEMARSG--RFDLILMDIKMPR 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 KKLNVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPE 73
                                                                                                                                                            CSTRAIN-ATCC 19089 / CBIS;
CSTRAIN-ATCC 19089 / CBIS;
CM MEDLINE-21173698; PubMed=11259647;
CM MEDLINE-21173699; PubMed=11259647;
CM MEDLINE-21173699; PubMed=11259647;
CM MEDLINE-21173699; PubMed=11259647;
CM MEDLINE-21173699; Pr., Alley M.R.K., Ohta M., Maddke N.D., Ely B., Roloney T., Dodson M.C., Navineha M.S., Gwinn M.L., Haft D.H.,
CALONEY T., Dodson M.C., Navineha M.S., Gwinn M.L., Haft D.H.,
CALONEY T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
Complete genome sequence of callboacter crescentus.";
Complete genome sequence of Callboacter crescentus.";
COMPLETE ACAG. SCI. U.S. A. 98:4136-4141(2001).
C. SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER REGILATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.

EMBL; AEG065980; AAKZ5124-1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=06.HI / CFT073 / ATCC 700928;
MEDLINE=22388244; Pubmed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
Extensive mosaic structure revealed by the complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Gaps
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Enterobacteriaceae; Escherichia.
NCBL_TaxID-217992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PSS0109; HIS_KIN; 1.
PROSITE; PSS0110; RESPONSE_REGULATORY; 1.
Kinase; Phosphorylation; Sensory transduction; Complete proteome.
SEQUENCE 394 AA; 41592 MW; 6D9AF0B278B70E70 CRC64;
Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
NCBI_TaxID=155892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49; Indels
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Sensor protein rcsC (EC 2.7.3.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match

25.7%; Score 174; DB 16;
Best Local Similarity 31.7%; Pred, No. 3.1e-07;
Matches 39; Conservative 31; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR005467; His_kinase.
InterPro; IPR001789; Response_reg.
Pfam; PF02518; HATPase_c; 1.
Pfam; PF0072; response_reg; 1.
SMART; SW0039; Response_reg; 1.
SMART; SW00448; REC; 1.
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SEQUENCE FROM N.A.
                                                    NCBI_TaxID=83334;
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Q8ZGR4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 VSTIKKLREMEVKS-----MIVGVISLADNEEERRAFMEAGLNHCLAKPLIKDKIIPLI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 VLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAV-IIHRDGGSSFDLILMDKEMPERDG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                         Gaps
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8
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01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last sentation update)
sensor for ctr capsule biosynthesis, probable histidine kinase
                                                                                                                                                                                                                                                                                                                                                                                       77 VSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKI 126
                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas stutzeri (Pseudomonas perfectomarina).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                    Length 949;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Graupper S., Wackernagel W.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ249741; CAB56474.1; -
InterPro; IPR002570; Hpt.
InterPro; IPR001789; Response_reg.
                                                                                          e; Complete proteome.
949 AA: 106590 MW; DF8CA47F9EEB4088 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER 1 1 1 SEQUENCE 417 AA; 45749 MW; D196B4FFDDA23BB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.1-May-2000 (TrEMBLrel. 13, Created)
0.1-May-2000 (TrEMBLrel. 13, Last sequence update)
0.1-Grave 1-2002 (TrEMBLrel. 22, Last annotation update)
putative histidine kinase (Fragment).
of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
EMBL; AE016763; AAN81215.1; ·
                                                                                                                                                                       DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25,5%; Score 173; DB 2; 32.8%; Pred. No. 4e-07;
                                                                                                                                                                 25.6%; Score 173.5; DB 10
33.6%; Pred. No. 9.7e-07;
iive 35; Mismatches 33.
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Kinase; Phosphorylation; Sensory transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35; Mismatches
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ProDon; P0000039; Response_reg; I.
SMART; SMO073; HPT; I.
SMART; SM0048; REC; I.
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nes 39; Conservative
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RCSC OR 23477 OR ECS3107.
Escherichia coli 0157:H7.
                                                                                                                                                                                                                               37; Conservative
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                                                                                                                                                                          Query Match
Best Local Similarity
Matches 37; Conserva
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                                                                                                                     SEQUENCE
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Matches
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Q9RLC7
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811 ILVVDDHPINRRLLADQLGSLGYQCKTANDGVDALNVL--SKNHIDIVLSDVNMPNMDGY 868
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MEDLINE-21156231; PubMed-11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino K., Ohnishi M., Murata T., Tanaka M., Tobe T., Tana C.-G., Ohtsubo E., Nakayawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli Oli5:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
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                                                                                                                                                                                                                                                           STRAIN=0157:H7, EDL933 / ATCC 700927;

MEDLINE=01074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Perna N.T., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R., Lin J., Yen G., Schwartz D.C.,

"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";

Nature 409:529-533(2001).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
101-MAR-2003 (TrEMBLrel. 23, Last annotation update)
101-MAR-2003 (TrEMBLrel. 23, Last annotation protein RcsC Two component sensor kinase/response regulator protein RcsC Two Corr. 20, 100 (EC 2.7.3.) (Sensor for ctr capsule biosynthesis).
101-MAR-2007 (101-MAR-20)
101-MAR-2003 (TREMBLR)
101-MAR-20
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33.9%; Pred. No. 1.4e-06;
Live 32; Mismatches 37
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PROSITE, PS50110; RESPONSE_REGULATORY; 1.
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SMART; SM00388: HiskA; 1.
SMART; SM00091; PAS; 1.
SMART; SM00448; REC; 1.
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Best Local Similarity 33.9%
Matches 37; Conservative
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us-09-646-679-15.rspt

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[1]
SEQUENCE FROM N.A.
SERQUENCE FROM N.A.
STRAIN=306 / ATCC 13902 / XV 101;
MEDLINE=22022145; PubMed=12024217;
MEDLINE=21142508; PubMed=11208780;
                                                                                              EMBL; AF319618; AAG60694.1;
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les 43; Conservative
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SEQUENCE STRAIN=KIM5 / Biovar Mediaevalis;

MEDINE-22137863; PubMed=12142430;

RA

Deng M., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,

RA

Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,

RA

Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,

RA

Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,

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Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,

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Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,

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Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,

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Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,

RA

STRAIN AMM6522.1;

REMBL; ALVI4147; CAC90055.1;

REMBL; ALVI3989; AAM86522.1;

RICEPPO; IPR003594; ATPbind_ATPase.

InterPro; IPR003561; His_kinas.

InterPro; IPR003661; His_kinas.

InterPro; IPR003661; His_kinas.

InterPro; IPR003661; His_kinas.

InterPro; IRR00399; Response_reg; 1.

PR PRIMTS; PR00312; HAYPASe_C; 1.

PR PRIMTS; PR0034; BCTRLEEWSOR.

BR PROSITE; PS0109; HIS_KIN; 1.

RW Kinase; Transferase; Complete procteome.

SQUENCE 957 AA; 108591 MW; 0447AIlF59100011 CRC64;
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                                                                  PERMINE-21470413; Pubmed-11586360; ParkINE-21470413; Pubmed-11586360; ParkINE-21470413; Pubmed-11586360; ParkINI J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebathia M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M., Chilingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Nature 413:523-527(2001).
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    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                 Enterobacteriaceae; Yersinia
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                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.2%; Score 171; DB 2; Length 927;
33.9%; Pred. No. 1.6e-06;
.ive 28; Mismatches 42; Indels 14; Gaps
Visick K.L., Skoufos L.M.;
"A two-component sensor required for normal symbiotic colonization of Euprymna scolopes by Vibrio fischeri.";
"5 Dacteriol. 183:835-84(2001).
                                                                                                                                                                                      --- SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0cr-2002 (TrEMBLrel. 22, Created)
01-0cr-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
TWO-component system sensor protein.
AACO494.
AAnthomona axonopodis (pv. citri).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadaeses:
Xanthomonadaeseae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                      R EMBL; AFILYBLE AAGROUGY 1.1;

R InterPro; IPR00359; Bact_sens_pr_C.

R InterPro; IPR00361; His_Kinase.

R InterPro; IPR00361; His_Kinase.

R InterPro; IPR003661; His_Kinase.

R InterPro; IPR001601; PAC.

R InterPro; IPR001000; PAS-assoc_C.

R Pfam; PF00512; His RA; I.

R Pfam; PF00512; His RA; I.

R Pfam; PF00512; His RA; I.

R Pfam; PF000785; PAC; I.

R Pfam; PF000785; PAC; I.

R Pfam; PF000785; PAC; I.

R PRNTS; RM0038; His RA; I.

R RMART; RM0038; His RA; I.

R RMART; RM0038; His RA; I.

R RMART; RM0039; PAC; I.

R RMART; RM0039; PAC; I.

R RMART; RM0044; RCC; I.

R RART; RM0044; RCCC; I.

R RART; RM0044; RC
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Quagqio R.B., Montairo-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
Alves L.M.C., Gannavan P.M., Bertolini M.C., Camargo L.B.,
Canactel G., Cannavan F., Cardozo J., Chambergo E.P.,
A locatell R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
A fara J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,
Ratia J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,
A katsuyama A.M., Kishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,
Ancall E.C., Meidando M.A., Madaira A.M. Miyaki C.Y., Moon D.H.,
Antins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
Morelra L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
Antino E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
Morelra L.M., Rossi A., Sena J.A.D., Silva C., Ge Souza R.F.,
Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
Stinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
Stinola L.A.F., Takita M.D., Silva C., White F.F.,
Schubal J.C., Kitajima J.D.,
Tundade dos Santos M., Truiffi D., Tsai S.M., White F.F.,
Schubal J.C., Meidanis J.J.,
Rature 417.459-463(2002).
Rature 417.459-463(2002).
Rature 417.459-463(2002).
Rature Ford IPRO04358; Bact_Sena_P.C.
Rature Ford IPRO04358; Bact_Sena_P.C.
RaterPro, IPRO04358; Bact_Sena_P.C.
RaterPro, IPRO04358; Bact_Sena_P.C.
RaterPro, IPRO04358; Rater Sena_P.C.
Rater Pro, Rater P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 KKLNVLIVDDDPLNLITHEKIİKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPE 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 RDGVSTTKKLREMEVKS-----MIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PERMIN-306 / ARCC 13902 / XV 101;

MEDLINE-22022145; PubMed-12024217;

da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,

Cicarpelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry-E.,

Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Xanthomonadaceae; Xanthomonas.
NCBL_TaxID=92829;
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Last annotation update)
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PRINES: PR00344; BCTRLSENSOR.
PR000019: Response_reg; 1.
PROSITE: PS50109; HIG_KIN: 1.
PROSITE: PS50110; RESPONSE_REGULATORY; 1.
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01-0CT-2002 (TrEMBLrel. 22, Last seq
01-MAR-2003 (TrEMBLrel. 23, Last anno
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XAC2492.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome.
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QG PONB

QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT QG DT 
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77 VSTTKKLREMEVKSM -- IVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLINQLM 134
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Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F., Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M., Martins E.C., Machadis J., Menck C.F.M., Miyaki C.Y., Moon D.H., Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R., Spinola L.M., Rossi A., Sena J.A.D., Silva C., de Souza R.F., Spinola L.A., Rossi A., Tamira R.B., Teixeira B.C., Tezza R.I.D., Sctubal J.C., Kitalima J.P.; Truidiade dos Santos M., Truifi D., Tsai S.M., White F.F., Tezza R.I.D., Comparison of the genomes of two Xanthomonas pathogens with differing Nature 417:459-46312002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Gaps
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MEDLINE=99047557; PubMed=9829920;
MEDLINE=99047557; PubMed=9829920;
Belas R., Schneider R., Melch M.;
"Characterization of Proteus mirabilis precocious swarming mutants: identification of rsbA, encoding a regulator of swarming behavior.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Proteus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.7%; Score 167.5; DB 16; Length 1364; 29.2%; Pred. No. 5e-06; Live 37; Mismatches 45; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1364 AA; 150282 MW; F7CCA3856B7E7165 CRC64;
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Last sequence update)
Last annotation update)
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Pfam: PF02318; HATPSSE_C: 1

Pfam: PF0218; HATPSSE_C: 1

Pfam: PF00167; Hiska; 1.

Pfam: PF00167; Hiska; 1.

Pfam: PF00189; PAC: 2.

Pfam: PF00189; PAC: 2.

Pfam: PF00189; PAC: 2.

Pfam: PF00172; Response_reg; 2.

PRNINTS: PR00134; BCTRLSENSOR.

PRODITE: PS50189; CHASE; 1.

PROSITE: PS50119; PAC: 2.

PROSITE: PS50119; PAC: 2.

PROSITE: PS50119; PAC: 2.

PROSITE: PS50110; RESPONSE_REGULATORY; 2.

COMPLETE PS50110; RESPONSE_REGULATORY; 2.

COMPLETE PS50110; RESPONSE_REGULATORY; 2.

COMPLETE PS50110; RESPONSE_REGULATORY; 2.
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                                                                                                                                                                                                                                                                                                                                                  EMBL, AE011887, AAM37343.1; -. EMBL, AE011887, AAM37343.1; -. InterPro; IPR001859, ATPbind, ATPase. InterPro; IPR001899, CHASE. InterPro; IPR001899, CHASE. InterPro; IPR001667, His.kina. InterPro; IPR001677, His.kinase. InterPro; IPR001610; PAC. InterPro; IPR001100, PAC. InterPro; IPR001010, PAC. InterPro; IPR001010, PAC. InterPro; IPR001014, PAS.domain. InterPro; IPR001014, PAS.domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 29.2*
Matches 35; Conservative
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RCsc,
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Search con
Job time
RESTRAINMENT OF STATE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 LNVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERD 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Gaps
                  -!- SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xanthomonas campestris (pv. campestris).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 GVSTTKKLREMEVKSMIVGVTSLADNEEERRAFWEAGLNHCLAKPLT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | :||: | :||: | |:||: | 455 GYQLATTVRELSSTIPIIGVTANAIAEEKQRC-IDAGMNDCVSKPVS 500
                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50110; RESPONSE_REGULATORY; 1.
Kinase; Phosphorylation; Sensory transduction; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24.6%; Score 166.5; DB 2; Length 36.4%; Pred. No. 1.9e-06; Live 26; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               F5DA2EAD9C35DEF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1364 AA
                                                            EMBL; AR071215; AAC82662.1; -...
HSSP; P06657; 2CHF.
InterPro: IPR003594; ATPbind_AMPRASE.
InterPro: IPR00358; Bact_Sens_Pr_C.
InterPro: IPR00368; H3c_MinA.
InterPro: IPR0036467; His_Kinase.
InterPro: IPR001789; Response_reg.
Ffam; P062012; H3KA; 1.
Pfam; PF00512; H3KA; 1.
Pfam; PF00012; HSKA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequ
01-MAR-2003 (TrEMBLrel. 23, Last anno
Two-component system sensor protein.
XCC2560.
                                                                                                                                                                                                                                                                         PRINTS; PR00344, BCTRLSENSOR.
ProDom; PD000039, Response_reg; 1.
SMART; SM00387, HATPRSe_c; 1.
SMART; SM00388; Hisks, 1.
  J. Bacteriol. 180:6126-6139(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 417:459-463(2002).
EMBL; AE012344; AAM41638.1; -.
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SEQUENCE 507 AA; 57326 MW;
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                                                 KINASES
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Matches
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Q8P883
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DR InterPro; IPR0043594; Arpbind_ATPase.

DR InterPro; IPR004359; Bact_Sens_Pr_C.

DR InterPro; IPR004567; His_Kinas.

DR InterPro; IPR00467; His_Kinas.

DR InterPro; IPR004189; Ass_Commin.

DR InterPro; IPR004189; Response_reg.

DR Pfam; PP07218; Hiska; I.

DR Pfam; PP07218; Hiska; I.

DR Pfam; PP07078; PAC; 2.

DR Pfam; PP07095; PAC; 2.

DR Pfam; PP07099; PAC; 2.

DR PR04118; PAC; 2.

DR PR05118; PAC; 2.

DR PR05118; PAC; 2.

DR PR05118; PAC; 2.

DR PR05118; PAC; 3.

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earch completed: August 14, 2003, 16:49:03 ob time : 98 secs

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Thu Aug '14 17:18:20 2003
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A nucleic acid encoding a signal transduction protein involved in plant dehiscence, useful for producing shatter resistant male sterile plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; dehiscence; male sterile plant; DZ2 gene; oilseed rape; response regulator protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brassica response regulator protein DZ2.
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AAB96490
                                                                                                                                                              AA026988
AA026987
AA026986
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AAB73276
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AAY28484
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ABG70785
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                                                                                    AA026994
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                                                                                                                                                                                         (first entry)
                                                             (BIOG-) BIOGEMMA UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wyatt P, Roberts JA,
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N-PSDB; AAZ22974.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal transduction shatter resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brassica napus.
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AAY42637;
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AAY42637
Arabidopsis thalia
Arabidopsis thalia
A. thaliana D22AT3
Brassica response
Arabidopsis,thalia
Arabidopsis thalia
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Brassica response
                                                                                        August 13, 2003, 19:06:41; Search time 41 Seconds (without alignments) 526.508 Million cell updates/sec
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| SIDSI/gcddata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDSI/gcddata/geneseq/geneseqp-embl/AA1981.DAT:*
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| SIDSI/gcddata/geneseqy-embl/AA1999.DAT:*
| SIDSI/gcddata/geneseqy-embl/AA2000.DAT:*
                                                                                                                                                                   1 MATKSMGDIEKIKKKLNVLI......LAKPLTKDKIIPLINQLMDA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                   1107863 seqs, 158726573 residues
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Maximum Match 100%
Listing first 45 summaries
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AAG10549
AAG44439
AAY42645
AAG10550
AAG44440
AAG21089
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    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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142
142
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70
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Match
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79.4
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Bucalyptus grandis
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Pseudomonas aerugi Pseudomonas aerugi

Pseudomonas aerug

Scoring table:

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Result

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Title: Perfect score:

sequence:

OM protein

Run on:

E. coll RscC recel Pseudomonas aerugi
Brassica napus DZ2

Pinus radiata cell

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sequence represents the B. napus DZ2 putative peptide sequence
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                                                                   Matches
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                                          The invention provides a nucleic acid encoding a signal transduction protein involved in the process of dehiscence. The nucleic acids and proteins are useful for requiating or controlling dehiscence of a pod or an anther in a plant, useful in the production of male sterile plants. The methods, etc. may be used in production of shatter resistance or shatter delayed plants such as oilseed rape (Brassica napus). The present sequence represents a B. napus response regulator protein D22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention provides a nucleic acid encoding a signal transduction protein involved in the process of dehiscence. The nucleic acids and proteins are useful for requiating or controlling dehiscence of a pod or an anther in a plant, useful in the production of male sterile plants. The methods, etc. may be used in production of shatter resistance or shatter-delayed plants such as oilseed rape (Brassica napus). The present
                                                                                                                                                                                                                                                         61 SFDLILMDKEMPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFWEAGLNHCLAKP 120
                                                                                                                                                                                                                                                                      1 MATKSMGDIEKIKKKENVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGS 60
                                                                                                                                                                                                                         A nucleic acid encoding a signal transduction protein involved in plant dehiscence, useful for producing shatter resistant male sterile plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal transduction protein; dehiscence; male sterile plant; DZ2 gene; shatter resistance; oilseed rape; response regulator protein.
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brassica response regulator protein DZ2 putative peptide seguence.
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0
                                                                                                                                                             100.0%; Score 678; DB 20; Length 135; 100.0%; Pred. No. 1e-67; ative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                     AAY42653 standard; Protein; 136 AA.
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                     Claim 4; Fig 1; 71pp; English.
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                                                                                                                                                                                     Conservative
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                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                       136 AA;
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Matches 136;
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                                                                                             1 MATKSMGDIEKIKKKLNVLIVDDDPLNLITHEKIIKAIGGISQTANNGEEAVIIHRDGGS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter termination sequence.
                                                              Gaps
                                                            ö
                              Length 136;
                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana protein fragment SEQ ID NO: 8916.
                          100.0%; Score 67%; DB 20;
100.0%; Pred. No. 1e-67;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                               AA.
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99US-0126785.
99US-0127462.
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99US-0131449.
99US-0132048.
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99US-0123180.
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99US-0125788.
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                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                            al Similarity 100.
136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana.
136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
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04-MAY-1999;
05-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                            17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-SEP-2000
Seguence
                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                             AAG10549;
                              Query Match
Best Local S
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		* ທ່ານ ທ່າງ ປ. ພ. ຈ. ທ. ປ. ປ. ຈ. ຈ. ໑. ໑. ໐. ໐. ໐. ໐. ໐. ໐. ໐. ໐. ໐. ໐. ໐. ໐. ໐.
18-0135253 19-0135252 18-0136622 18-0136021 19-013722 18-013722 18-0137508 18-0137508 18-0138640 18-0139452 18-0139452 18-0139452	0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (0.00 (9990S-0144005. 990S-0144005. 990S-01444325. 990S-0144331. 990S-0144333. 990S-0144333. 990S-0144333. 990S-0144335. 990S-0144335. 990S-0144335. 990S-0145086. 990S-0145089. 990S-0145189. 990S-0145189. 990S-0145189. 990S-0145189. 990S-0145189. 990S-0145189. 990S-0145189. 990S-0145189.
-MAY 11999 -MAY 11999 -MAY 11999 -MAY 11999 -JUN 11999	100 100 100 100 100 100 100 100 100 100	14-701-1999; 16-701-1999; 16-701-1999; 19-701-1999; 19-701-1999; 19-701-1999; 19-701-1999; 20-701-1999; 20-701-1999; 21-701-1999; 22-701-1999; 22-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999; 23-701-1999;
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PR 02-MG-1999; 99US-014638B.

PR 03-MG-1999; 99US-0147204

PR 04-MG-1999; 99US-0147204

PR 04-MG-1999; 99US-0147204

PR 04-MG-1999; 99US-0147192

PR 05-MG-1999; 99US-0147192

PR 10-MG-1999; 99US-0147192

PR 10-MG-1999; 99US-014716

PR 11-MG-1999; 99US-014716

PR 11-MG-1999; 99US-014716

PR 12-MG-1999; 99US-014911

PR 11-MG-1999; 99US-014912

PR 12-MG-1999; 99US-014912

PR 12-MG-1999; 99US-014912

PR 23-MG-1999; 99US-015066

PR 23-MG-1999; 99US-0151066

PR 23-MG-1999; 99US-0151300

PR 23-MG-1999; 99US-0150300

PR 23-MG-1999; 99US-015000

PR 23-MG-1999; 99US-015000

PR 23-MG-1999; 99US-015000

PR 23-MG-1999; 99US-015000

PR 23-MG

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55 HRDGGSSFDLILMDKEMPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLN 114
                                                                                                                                                                                                   1 MATKSMGDIEK ----IKKKL-NVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVII 54
                                                                                                                                                                                                                                 1 MATKSIGGTEKTKSIEVKKKLINVLIVDDDPLNRRLHEMIIKTIGGISQTAKNGEEAVIL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                 Gaps
                                                                                                                                                              9
                                                                                                             Query Match 79.4%; Score 538; DB 21; Length 142; Best Local Similarity 78.9%; Pred. No. 4.7e-52; Matches 112; Conservative 8; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana protein fragment SEQ ID NO: 55668.
                                                                                                                                                                                                                                                                                                                                                                                   AAG44439 standard; Protein; 142 AA.
  99US-0161920.
99US-0161992.
99US-0161993.
99US-0162142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9905-0121825.
9905-0123180.
9905-0123180.
9905-0125788.
9905-01267824.
9905-01284134.
9905-0132485.
9905-0132486.
9905-0132486.
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9905-0132486.
9905-0132486.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana.
28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
29-0CT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-APR-1999;
30-APR-1999;
04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 - MAY - 1999;
14 - MAY - 1999;
18 - MAY - 1999;
19 - MAY - 1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP1033405-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-APR-1999;
28-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAY-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG44439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
AAG44439
ID AAG44439
ID AAG4439
ID AAG4
XX AAG4
XX AAG4
XX AAG4
XX BC AAG6
XX BC ACC
XX
  g
                                                                                                                                                                                                                                                                                                                                                                                                                              q
                                                                                                                                                                                                                                                                                          δ
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990S-0144884.
990S-0144884.
990S-0145086.
990S-0145088.
                                                                                                                                                                        99005 - 0139455
99005 - 0139455
99005 - 0139455
99005 - 0139456
99005 - 0139465
99005 - 0139460
99005 - 0139460
99005 - 0139461
99005 - 0139463
99005 - 0139463
                                                                                                                                                                                                                                                                                                                                                                                   99US - 0140991
99US - 0141287
99US - 0141287
99US - 0142154
99US - 0142390
99US - 0142390
99US - 0142977
99US - 0142977
99US - 0143624
99US - 0144086
99US - 0144332
99US - 0144333
                               990S-0136021.
990S-0136392.
990S-0137222.
990S-0137528.
990S-0137524.
                                                                                                                    990S-0138540.
990S-0138847.
990S-0139119.
990S-0139452.
                                                                                                                                                                                                                                                                                                                                                   99US-0140354.
99US-0140695.
99US-0140823.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                990S-0145089.
990S-0145192.
990S-0145145.
990S-0145218.
990S-0145224.
99US-0135124.
99US-0135353.
99US-0135629.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0145918.
99US-0145919.
99US-0145951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0145087
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PR 02-MC-1999; 9905-0146386.

PR 02-AUG-1999; 9905-0146388.

PR 03-AUG-1999; 9905-0147038.

PR 04-AUG-1999; 9905-0147038.

PR 04-AUG-1999; 9905-0147038.

PR 05-AUG-1999; 9905-0147122.

PR 05-AUG-1999; 9905-0147123.

PR 05-AUG-1999; 9905-0147133.

PR 10-AUG-1999; 9905-0147133.

PR 10-AUG-1999; 9905-0147133.

PR 11-AUG-1999; 9905-0147133.

PR 11-AUG-1999; 9905-0148341.

PR 12-AUG-1999; 9905-014926.

PR 12-AUG-1999; 9905-014926.

PR 22-AUG-1999; 9905-014926.

PR 22-AUG-1999; 9905-014926.

PR 23-AUG-1999; 9905-014922.

PR 23-AUG-1999; 9905-014926.

PR 23-AUG-1999; 9905-014926.

PR 23-AUG-1999; 9905-014926.

PR 23-AUG-1999; 9905-014926.

PR 23-AUG-1999; 9905-0114938.

PR 24-SEP-1999; 9905-0114938.

PR 22-SEP-1999; 9905-0114938.

PR 24-SEP-1999; 9905-0114938.

PR 24-SEP-1999; 9905-0114938.

PR 11-CCT-1999; 9905-0114938.

PR 11-CCT-1999; 9905-0114938.

PR 11-CCT-1999; 9905-0114938.

PR 113-CCT-1999; 9905-0118389.

PR 21-CCT-1999; 9905-0118389.
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The invention provides a nucleic acid encoding a signal transduction protein involved in the process of dehiscence. The nucleic acids and proteins are useful for regulating or controlling dehiscence of a pod or an anther in a plant, useful in the production of male sterile plants. The methods, etc. may be used in production of shatter resistance or shatter-delayed plants such as oilseed rape (Brassica napus). The present sequence represents a D22 A. thaliana homologue D22AT3 putative peptide sequence.
                                                                                                                                                                          55 HRDGGSSFDLILMDKEMPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLN 114
                                                                                                                                                                                        61 HRDGEASFDLILMDKEMPERDGVSTTKKLREMKVTSMIVGVTSVADGEEERKAFMEAGLN 120
                                                                                                                                                   9
                                                                                                                            54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A nucleic acid encoding a signal transduction protein involved in plant dehiscence, useful for producing shatter resistant male sterile plants
                                                                                                                          1 MATKSMGDIEK----IKKKL-NVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVII
                                                                                                                                         Gaps
                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                             Signal transduction protein; dehiscence; male sterile plant; shatter resistance; oilseed rape; DZ2AT3 gene.
                                                                         Length 142;
                                                                                                    16; Indels
                                                                         Score 538; DB 21;
Pred. No. 4.7e-52;
8; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                      A. thaliana DZ2AT3 putative peptide sequence.
                                                                                                                                                                                                                                                 Location/Qualifiers
Misc-difference 57
                                                                                                                                                                                                                                  HCLAKPLTKDKIIPLINQLMDA 136
                                                                                                                                                                                                                                                                                                                           AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Whitelaw C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "unknown"
88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Fig 9; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "unknown"
                                                                                                                                                                                                                                                                                                                          AAY42645 standard; Protein; 142
99US-0161361.
99US-0161920.
99US-0161992.
99US-0161993.
                                                                          Query Match 79.4%;
Best Local Similarity 78.9%;
Matches 112; Conservative &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-GB00905.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98GB-0006113.
                                                                                                                                                                                                                                                                                                                                                                              10-JAN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BIOG-) BIOGEMMA UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wyatt P, Roberts JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-580449/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAZ22978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09949046-A1.
 26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-SEP-1999
                                                                                                                                                                                                                                    115
                                                                                                                                                                                                                                                                                                                                                     AAY42645;
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                                                                                                                                                                                   55 HRDGGSSFDLILMDKEMPERDGVSTTKKLREMEVKSMIVGVISLADNEEFRRAFMEAGLN 114
                                                                                                     1 MATKSMGDIEK----IKKKL-NVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVII 54
                                                                                                                         A nucleic acid encoding a signal transduction protein involved in plant dehiscence, useful for producing shatter resistant male sterile plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal transduction protein; dehiscence; male sterile plant; D22B gene; shatter resistance; oilseed rape; response regulator protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 69.6%; Score 472; DB 20; Length 116; Best Local Similarity 80.2%; Pred. No. 8.4e-45; Matches 93; Conservative 11; Mismatches 12; Indels 0; Gaps
                                                                          6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                               Brassica response regulator protein DZ2B putative peptide sequence.
                                         76.0%; Score 515; DB 20; Length 142; 76.1%; Pred. No. 1.7e-49; ive 8; Mismatches 20; Indels 6
                                                                                                                                                                                                                                             121 HCLEKPLTKAKIFPLISHLFDA 142
                                                                                                                                                                                                                           115 HCLAKPLTKDKIIPLINQLMDA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                   AAY42652 standard; Protein; 116 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Whitelaw C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 2; Fig 6; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98GB-0006113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-GB00905.
                                                                                                                                                                                                                                                                                                                                                                                              10-JAN-2000 (first entry)
                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BIOG-) BIOGEMMA UK LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wyatt P, Roberts JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-580449/49.
N-PSDB; AA222976.
                                                     Best Local Similarity
Matches 108; Conserv
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                                                    81 KKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLINQLMDA 136
                                                                                                                                                                                Arabidopsis thaliana protein fragment SEQ ID NO: 8917
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Query Match 64.5%; Score 437; DB 21; Length 104; Best Local Similarity 84.5%; Pred. No. 5.9e-41; Matches 87; Conservative 5; Mismatches 10; Indels 0; Gaps

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                                                                                                                                                                     AAG44440 standard; Protein; 104 AA.
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                                                                                                                                                                                                            AAG44440;
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                                                                                                                                  RESULT 8
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
62 GYTSVADQEEERKAFWEAGLNHCLEKPLTKAKIFPLISHLFDA 104
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990S-01301449
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                                                                                                                                       Arabidopsis thaliana
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23.APR-1999;
28.APR-1999;
30.APR-1999;
30.APR-1999;
04.MAY-1999;
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14 - MAY - 1999;
14 - MAY - 1999;
14 - MAY - 1999;
19 - MAY - 1999;
20 - MAY - 1999;
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24-MAY-1999;
25-MAY-1999;
27-MAY-1999;
                                                                                                                                                      EP1033405-A2
                                                                                                                                                                      06-SEP-2000
                                                             AAG21089;
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                                RESULT 9
                                               34 IIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGVSTTKKLREMEVKSMIV 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 IIKTIGGISQTAKNGEBAVILHRDGEASFDLILMDKEMPERDGVSTTKKLREMKKYSMIV 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match

64.5%; Score 437; DB 21; Length 104;

Best Local Similarity 84.5%; Pred. No. 5.9e-41;

Matches 87; Conservative 6; Mismatches 10; Indels
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31-Aug-1999;
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10-SEP-1999;
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0139455 0139455 0139460 0139460 0139461 0139460 0139750 0139763 0139817	S-0140354. S-0140354. S-0140893. S-0141287. S-0141287. S-0141287. S-0142803. S-0142803. S-0142803. S-0142803. S-0144862. S-0144085. S-0144328. S-0144333. S-0144333.	00144444444444444444444444444444444444	00146338 00146338 0014703 0014703 0014703 0014719 001473 0014743 0014743 0014817 0014834 0014834 0014834 0014834 0014834 0014834
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9903-0145087.
9903-0145089.
      Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                 17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                Arabidopsis thaliana
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                   Arabidopsis thaliana protein fragment SEQ ID NO: 23517.
AAG21088 standard; Protein; 71 AA.
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                         17-OCT-2000 (first entry)
                                                                          Arabidopsis thaliana.
                                                                                                 06-SEP-2000
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990S-0161920.
990S-0161993.
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25 - SEP - 1999;

06 - OCT - 1999;

07 - OCT - 1999;

08 - OCT - 1999;

13 - OCT - 1999;

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16 - OCT - 1999;

17 - OCT - 1999;

18 - OCT - 1999;

21 - OCT - 1999;

21 - OCT - 1999;

22 - OCT - 1999;

25 - OCT - 1999;

26 - OCT - 1999;

27 - OCT - 1999;

28 - OCT - 1999;

29 - OCT - 1999;
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Best Local S:
Matches 55
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99US-0139459.
99US-0139460.
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0; Gaps

71 MPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFWEAGLNHCLAKPLTKDKIIPLI 130

131 NQLMDA 136 SHLFDA 66

61

RESULT 11 AAG21088

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	DB 21; Length 71; .7e-16; sendth 71; es 8; Indels 6; Gaps 2; LNLIHEKIIKAIGGISOTANNGEBAVII 54 :		
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PR 23-AUG-1999; PR 25-AUG-1999; PR 27-AUG-1999; PR 27-AUG-1999; PR 27-AUG-1999; PR 30-AUG-1999; PR 30-AUG-1999; PR 31-AUG-1999; PR 10-SEP-1999; PR 11-SEP-1999; PR 11-SEP-1999; PR 22-SEP-1999; PR 22-SEP-1999; PR 24-SEP-1999; PR 25-SEP-1999; PR 25-SEP-1999; PR 25-SEP-1999; PR 25-SEP-1999; PR 25-SEP-1999; PR 26-SEP-1999; PR 28-SEP-1999;	Ouery Match Best Local Simila Matches 47; Co Oy 1 MATKS	Qy 55 HRDG Db 61 HRDG	RESULT 12 AAB25159 ID AAB25159 standar XX AC AAB25159;

(first entry)

27-NOV-2000

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AAA TAJ263 to AAA79736 and AAB25100 to AAB25570 represent polynucleotide
and protein sequences isolated from eucalyptus (Eucalyptus grandis) or
pine (Pinus radiata also known as Monterey pine). The protein sequences
are involved in cell signalling. The polynucleotide and protein
sequences can be used to modify the response of plant cells to external
sequences can be used to modify cell protein
sequences can be used to modify cell proliferation,
development of a plant. They can be used to modify cell proliferation,
development of a plant. They can be used to modify cell proliferation,
development of a plant. They can be used to modify cell proliferation,
attered fruit ripening and senescence of leaves and flowers e.g. to
altered fruit ripening and senescence of leaves and flowers e.g. to
delay senescence and prolong the life of cut flowers or enhance
senescence of reproductive organs to engineer sterile plants. Other
modifications can be used to delay senescence in selected cell types or
organs providing fruit and vegetables which have a longer shelf life
between harvest and consumption, or to decrease branching frequency in
consume the species giving long stretches of valuable knot-free clear
consumers and prolong the limber furniture and veneers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated polynucleotide encoding a polypeptide involved in cell signaling used for generating transgenic plants with modified responses
                                                                                     Eucalyptus grandis; Pinus radiata; Monterey pine; plant; modification; plant cell signalling; modulation; transgenic plant; pathogen; growth; environmental change; development; cell proliferation; differentiation; elongation; survival; disease resistance; nutrient metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
29.8%; Score 202; DB 21; Length 261;
Best Local Similarity 36.5%; Pred. No. 3.7e-14;
Matches 42; Conservative 34; Mismatches 37; Indels
                                                    Pinus radiata cell signalling involved protein SEQ ID NO:127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  claim 3; Page 104-105; 527pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                          (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY42644 standard; Protein; 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strabala TJ, Nieuwenhuizen NJ;
                                                                                                                                                                                                                                                                                                                        11-JAN-2000; 2000WO-US00724
                                                                                                                                                                                                                                                                                                                                                               99US-0228986
99US-0162866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to external signals -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  261 AA;
                                                                                                                                                                                                                                           WO200042171-A1
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                                                                                                                                                                                                   Pinus radiata
                                                                                                                                                                                                                                                                                                                                                                 12-JAN-1999;
01-NOV-1999;
                                                                                                                                                                                                                                                                                  20-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY42644;
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ID AAY4
XX AAY4
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The invention provides a nucleic acid encoding a signal transduction protein involved in the process of dehiscence. The nucleic acids and proteins are useful for regulating or controlling dehiscence of a pod or an arther in a plant, useful in the production of male sterile plants. The methods, etc. may be used in production of shatter resistance or shatter-delayed plants such as oilseed rape (Brassica napus). The present sequence represents the partial fragment of B. napus D22B protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RscC; antagonist; agonist; cytokinin receptor; receptor; signal transduction; histidine kinase; hormone; cell division; cell differentiation; agriculture; growth regulator; harvest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAT--KSMGDIEK----IXKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVI 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A nucleic acid encoding a signal transduction protein involved in plant dehiscence, useful for producing shatter resistant male sterile plants
                                 Signal transduction protein; dehiscence; male sterile plant; D22B gene; shatter resistance; oilseed rape; response regulator protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 28.4%; Score 192.5; DB 20; Length 67; Best Local Similarity 65.7%; Pred. No. 6.7e-14; Matches 44; Conservative 6; Mismatches 10; Indels 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E. coli RscC receiver region of histidine kinase.
      Brassica napus DZ2B partial fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABG70785 standard; Protein; 118
                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Fig 5; 71pp; English.
                                                                                                                                                                                                                                                                  Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-MAR-2002; 2002EP-0005749.
                                                                                                                                                                                                        98GB-0006113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-DEC-2002 (first entry)
                                                                                                                                                                                                                                  (BIOG-) BIOGEMMA UK LTD.
                                                                                                                                                                                                                                                                  Roberts JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 IHRDGGS 60
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                                                                                                                                                                                                                                                                                                 WPI; 1999-580449/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli
                                                                                                                                                                                                                                                                                                               N-PSQB; AA222975
                                                                                     Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP1241182-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-SEP-2002
                                                                                                                  WO9949046-A1
                                                                                                                                                                            22-MAR-1999;
                                                                                                                                                                                                        20-MAR-1998;
                                                                                                                                             30-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABG70785;
                                                                                                                                                                                                                                                                  Wyatt P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 VLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 STIKKLREMEVKSMIVGVISLADNEEERRAFMEAGLNHCLAKPLIKDKIIPLINQ 132
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06-JUL-2001; 2001US-303286P. 16-APR-2002; 2002US-373233P. 05-JUL-2002; 2002WO-US23242

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The invention discloses a method for analysing antagonist or agonist activity to a cytokinin receptor. The method comprises bringing a candidate substance into contact with a transformed cell, in which a encoding the receptor has been introduced, and then measuring the existence, or the quantity, of the intracellular signal transduction from the receptor expressed in the cell. The cytokinin receptor comprises an extracellular region of the receptor, transmembrane regions, a histidine kinase region and a receiver region of the kinase. The transmembrane receptor regions and kinase region of the monogeneous to each other and the receptor region is heterogeneous to them. Cytokinins are plant hormones relevant to cell division and differentiation of higher plants. The method is used for analysing agonist or antagonist activity to a cytokine receptor. A substance with agonist or antagonist activity to the receptor can be used in agriculture, as a plant growth regulator, e.g. after harvest. The advantage is that the candidate substances do not need to be prepared in such large amounts as in previous methods and that the method avoids the immensely long time to observe and evaluate the growth of the plant candidate substances of the proparation of histidine kinase which can be resented is the E. coli receiver region of histidine kinase which can transmit signals to the cytokinin receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 VLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Antibacterial; PvrR; variant Pseudomonas; microorganism; gram negative;
phenotype-mediated antibiotic-resistance; gram-positive;
                                                                                                                                                                                                                 Analyzing agonist or antagonist activity of a substance for use as a plant growth regulator, comprises measuring intracellular signal transduction from a cytokinin receptor expressed in a cell contacted with the test substance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 25.3%; Score 171.5; DB 23; Length Best Local Similarity 33.9%; Pred. No. 3.2e-11; Matches 37; Conservative 32; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa PvrR related protein, SEQ ID No 4.
                                                                                                                                                                                                                                                                                                                   Disclosure; Page 42; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA026983 standard; Protein; 471 AA
                                                                                             SUMO ) SUMITOMO CHEM CO LID.
             15-MAR-2001; 2001JP-0073812.
29-JUN-2001; 2001JP-0198639.
29-JUN-2001; 2001JP-0198640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                  Higuchi M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bacterial infection
                                                                                                                                                                              WPI; 2002-693041/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003004691-A2.
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                                                                                                                                       Kakimoto I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAO26983;
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3; Gaps

DB 23; Length 118;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel isolated polypeptide comprising a PvrR (variant Pseudomonas) amino acid sequence having at least 50 % identity to a 399 residue amino acid sequence, given in the specification, where expression of the polypeptide, in a microorganism, affects phenotypemediated antibiotic resistance in the microorganism. The methods and compositions of the present invention are useful for the diagnosis, prevention and treatment of gram negative or gram-positive bacterial infection. This sequence represents a Pseudomonas protein used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated PurR polypeptide and polynucleotide that regulates bacterial biofilm formation, useful for the diagnosis, prevention and treatment of gram-negative or gram-positive bacterial infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43; Indels
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he : 43 secs
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                                                                                                                                                                                                                                                      (GEHO ) GEN HOSPITAL CORP.
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Matches 38; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-221608/21.
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                                                                                                                                                                                                                                                                                                                                           Ausubel FM,
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Sequence 127, App
Sequence 31338, A
Sequence 21359, A
Sequence 20395, A
Sequence 26, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 220, App
Sequence 2512, Appl
Sequence 2512, Appl
Sequence 2512, Appl
Sequence 26112, A
Sequence 26112, A
Sequence 26112, A
Sequence 27075, A
Sequence 18607, A
Sequence 18607, A
Sequence 18607, A
Sequence 27075, A
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                                                                                                                     August 13, 2003, 19:10:32 ; Search time 17 Seconds (without alignments) 338.487 Million cell updates/sec
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678
1 MATKSMGDIEKIKKKLNVLI......LAKPLTKDKIIPLINQLMDA 136
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-225-991A-1138
US-09-252-991A-1138
US-09-252-991A-20395
US-09-252-991A-20395
US-09-252-991A-7557
US-08-843-530B-36
US-08-843-530B-3
US-08-843-530B-3
US-08-843-530B-3
US-08-843-530B-3
US-08-843-530B-3
US-09-252-991A-28943
US-09-252-991A-28943
US-09-252-991A-2895
US-09-252-991A-18607
US-09-252-991A-18607
US-09-252-991A-18607
US-08-843-530B-18
US-08-843-530B-18
US-08-843-530B-18
US-08-843-530B-18
US-08-9252-991A-1868
US-09-252-991A-18607
US-09-252-991A-18607
US-09-252-991A-18607
US-09-252-991A-18607
US-09-252-991A-1868
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                                                                                                                                                                                                                                                                                                                                                             328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                  using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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No.
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Sequence 6073, Ap Sequence 22932, A Sequence 22216, A Sequence 23167, A Sequence 23765, Ap Sequence 114, App Sequence 19564, A Sequence 6859, Ap Sequence 6859, Ap Sequence 61746, Ap Sequence 5430, Ap Sequence 5430, Ap Sequence 5430, Ap Sequence 3779, Ap Sequence 5430, Ap Sequence 5430, Ap Sequence 221, App		ant Cells ition of Plant Cell Signalling	Length 261;); Indels 2; Gaps 2;	VLIVDDDPLNLITHEKIIKAIGGISGTANNGEEAVITHRDGGSSFDLILMDKEMPERDGY 77 : : :	ND AMINO ACID SEQUENCES RELATING TO ACINETOBACTE DIAGNOSTICS AND THERAPEUTICS
US-09-328-352-6073 US-09-252-991A-22932 US-09-252-991A-22216 US-09-252-991A-31677 US-09-328-352-6809 US-09-252-991A-31677 US-09-252-991A-1345 US-09-252-991A-16981 US-09-252-991A-17904 US-09-252-991A-17904 US-09-252-991A-17904 US-09-328-352-6430 US-09-328-352-5430 US-09-328-352-5430 US-09-328-352-5430 US-09-328-352-5430 US-09-328-352-5430 US-09-328-352-5430 US-09-328-352-5430	ALIGNMENTS	09228986 ls Isolated from Plant (r Use in the Modification US/09/228,986 -12 s Version 3.0	; Score 202; DB 4; ; Pred. No. 7e-16; 34; Mismatches 37	IIKAIGGISQTANNGEEAVIIHRDGGSSFDLILL	//09328352 al. ACID AND AMINO ACID & I FOR DIAGNOSTICS AND US/09/328,352
18.1 17.6 17.6 17.6 17.6 17.6 17.6 17.6 17.6 17.6 17.6 18.7 18.8 18.4 18.7 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9 18.9		RESULT 1 US-09-228-986-127 Sequence 127, Application US/09228986 Settle No. 6359198 GENERAL INFORMATION: APPLICANT: Strabala, Timothy APPLICANT: Strabala, Timothy TITLE OF INVENTION: and Their Use in the TITLE OF INVENTION: and Their Use in the FILE REFERENCE: 11000/1020 CURRENT APPLICATION NUMBER: US/09/228, 9 CURRENT FILING DATE: 1999-01-12 NUMBER OF SEQ ID NOS: 130 SOFTWARE: FASTSEQ for Windows Version 3 SEQ ID NO 127 SEQ ID NO 127 ILENGTH: 261 TYPE: PRT ORGANIEM: Phus radiata	E 0.14		RESULT 2 US-09-328-352-7973 Sequence 7973, Application US/0932835 Patent No. 656298 GENERAL INFORMATION: APPLICANT: GATY L. Breton et al. TILLE OF INVENTION: NUCLEIC ACID AND FILLE OF INVENTION: NACLEIC ACID AND FILE REFERENCE: GTC99-03PA CURRENT APPLICATION NUMBER: US/09/32 CURRENT APPLICATION NUMBER: US/09/32 SEQ ID NO 7973 LENGTH: 946 TYPE: PRT ORGANISM: Acinetobacter baumannii US-09-328-352-7973
28 122.5 30 120.5 31 110.2 32 1119 33 1119 34 112.5 36 112.5 37 112.5 38 111.5 39 111.5 40 110.5 42 1099 43 109.5 45 109.5		RESULT 1 US-09-228-986. Sequence 127 Sequence 127 Sequence 127 Sequence 127 Partent No. 6 APPLICANT: APPLICANT	Query Matc Best Local Matches	OY 18 Db 137 OY 78 Db 196	RESULT 2 US-09-328-352- Sequence 797 Patent No. 6 GENERAL INFO TITLE OF INFO TITLE DEAT TITLE OF INFO TITLE DEAT TITLE OF INFO TITLE DEAT TITLE ORGANISM: US-09-328-352-

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APPLICAT: MAIC J. RUBenfield et al.
APPLICAMT: MAIC J. RUBenfield et al.
APPLICAMT: MAIC J. RUBENFICAMION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196 13 156
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,190
PRIOR PILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20395
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Sequence 36, Application US/08843530B
Setent No. 5939306
GENERAL INFORMATION:
APPLICANT: Selitrennikoff, Claude
APPLICANT: Alex, Lisa A.
APPLICANT: Simon, Melvin I.
TITLE OF INVENTION: Osmosensing Histidine Kinases
NUMBER OF SEQUENCES: 36
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31.9%; Pred. No. 3.3e-08;
tive 26; Mismatches 45
                                                                                                                                                                                     21.8%; Score 148; DB 4;
28.8%; Pred. No. 1.1e-08;
iive 33; Mismatches 43;
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220 Montgomery Street, Suite 2200
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Sequence 20395, Application US/09252991A
Patent No. 6551795
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: United States of America
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                                                              TYPE: PRT
CRGANISM: Pseudomonas aeruginosa
US-09-252-991A-29359
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Matches 37; Conservative
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Matches 34; Conservative
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ADDRESSEE: Medlen & (
STREET: 220 Montgome:
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SEQ ID NO 29359
LENGTH: 947
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APPLICANT: MATC J. Rubenfield et al.

APPLICANT: MATC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEEC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEEC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/094,788

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                        674 LHILAVDDHLPNLIVLEALLGELNVKTTKALSGQEALNITQERIDQKLKPFDLVFMDIQM 733
                                                                                                                                                                                                                                                                                                                                           72 PERDGVSTTKKLREM-----EVKSMIVGVT--SLADNEBERRAFMEAGLNHCLAKPLTK 123
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                                                                                                                                                                       16 ENVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSS----FDLILMDKEM 71
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22.1%; Score 150; DB 4; Length 1014;
Best Local Similarity 25.5%; Pred. No. 7.4e-09;
Matches 35; Conservative 36; Mismatches 56; Indels 19
                                      Length 946;
                                      Query Match 22.5%, Score 152.5; DB 4; Length Best Local Similarity 30.2%; Pred. No. 3.4e-09; Matches 39; Conservative 34; Mismatches 41; Indels
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Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31338
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61 SFDLILMDKEMPERDGVSTTKKLREME-----VKSMIVGVTSLADNEEERRAFMEAGLNH 115
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                                               95 EATRLIRREERAQGWPRVPIVALTAHILD--EHRRAGIEAGMDAYLGKPVDRAELYATLE 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1281;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMENTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,530B
FILING DATE: 16-APR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                        Osmosensing Histidine Kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
20.6%; Score 139.5; DB 2;
Best Local Similarity 31.1%; Pred. No. 1.8e-07;
Matches 42; Conservative 28; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                        APPLICANT: Selitrennikoff, Claude
APPLICANT: Agnan, Jacqueline
APPLICANT: Agnan, Lisa A.
APPLICANT: Simon, Melvin I.
TITLE OF INVENTION: Osmosensing Histi
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 33.0
REFERENCE/DOCKET NUMBER: UTC-02717
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 765-8410
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 220 Montgomery Street, Su
CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08843530B Patent No. 2939306 GENERAL INFORMATION: APPLICANT: Selitrennikoff, Claude
                                                                                                                                                                                                                                                          Sequence 6, Application US/08843530B Patent No. 5939306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1188 YLSKPLOONHLIQTI 1202
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LENGTH: 1281 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                     132 QLM 134
                                                                                                                                               153 RLL 155
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US-08-843-530B-2
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GENERAL INCRMATION:
GENERAL INCRMATION:
APPLICANT:
MARC J. RUDEDITIED & al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17557
LENGTH: 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1080 DDDKNETSVKILVVEDNHVN----QEVIKRMLNLEGIENIELACDGQEAFDKVKELTSKG 1135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 VLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 21.4%; Score 145; DB 2; Length 1220; Best Local Similarity 29.0%; Pred. No. 3.8e-08; Matches 40; Conservative 40; Mismatches 44; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.2%; Score 144; DB 4; Length 162; 30.9%; Pred. No. 2.6e-09; ive 28; Mismatches 49; Indels
COMPUTER: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/843,530B
FILING DATE: 16-APR-1997
ATTORNEY APPLICATION: 435
                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: MacKnight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET UNDBER: UTC-02717
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 705-8410
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17557, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1195 KPIKRPKLKTILTEFCAA 1212
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US-09-252-991A-17557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 KPLTKDKIIPLINQLMDA 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1220 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid STRANDEDNESS: not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 38; Conserv
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US-09-252-991A-17557
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STREET: 220 Montgomery Street, Su:
CITY: San Francisco
STATE: California
COUNTRY: United States of America
21P: 94104
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MDIUM TYPE: Floppy disk
CMEDUWTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS_DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: MacKhight, Kamrin T.
REGISTRATION NUMBER: 38,230
REFERENCE/DOCKET NUMBER: UTC
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:||| :: :| |
1188 YLSKPLQQNHLIQTI 1202
                                                                                                                                                                                                                                                                                                                                        not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 CLAKPLTKDKIIPLI 130
                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: peptide US-08-843-530B-4
                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 16 CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 ATKSMGDIEKIKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAV-IIHRDGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1298;
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL AND AGAIN, Jacqueline
APPLICANT: Alax, Lisa A.
APPLICANT: Simon, Melvin I.
TITLE OF INVENTION: Osmosensing Histidine Kinases
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                   TITLE OF INVENTION: Osmosensing Histidine Kinases NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Monitoomery Street, Suite 2200
CITY: San Francisco
STATE: Callfornia
                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,530B
FILING DATE: 16.APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
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STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.6%; Score 139.5;
31.1%; Pred. No. 1.8e
tive 28; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1.188 YLSKPLQQNHLIQTI 1202
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 Agnan, Jacqueline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 CLAKPLTKDKIIPLI 130
                 Alex, Lisa A.
Simon, Melvin I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 31.1%
Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: peptide US-08-843-5308-2
                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1298 amir
TYPE: amino acid
STRANDEDNESS: no
                                                                                                                                                                                  COUNTRY: Ur
ZIP: 94104
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
US-08-843-530B-4
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61 SFDLILMDKEMPERDGVSTTKKLREME-----VKSMIVGVTSLADNEEERRAFMEAGLNH 115
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                                                                                                                                                                                                                                                                                                                                                                                               Query Match
20.6%; Score 139.5; DB 2; Length 1298;
Best Local Similarity 31.1%; Pred. No. 1.8e-07;
Matches 42; Conservative 28; Mismatches 52; Indels 13;
APPLICANT: Selitrennikoff, Claude
APPLICANT: Agnan, Jacqueline
APPLICANT: Alex, Lisa A.
APPLICANT: Alex, Lisa A.
APPLICANT: Simon, Melvin I.
TITLE OF INVENTION: Osmosensing Histidine Kinases
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMedien & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/843,530B FILING DATE: 16 APR-1997
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APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 107196.118

FULLE REPERENCE: 107196.118

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR PAPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 25928

LENGTH: 760
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 STIKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLIKDKIIPLINQL 133
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                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 20.4%; Score 138.5; DB 4; Length 234; Best Local Similarity 30.2%; Pred. No. 2e-08; Matches 35; Conservative 31; Mismatches 47; Indels 3
                                APPLICANT: "C'ITOLE", Paul W. APPLICANT: Reid, Julian R. APPLICANT: Reid, Julian R. APPLICANT: Colbear, Timothy TITLE OF INVENTION: Polynucleotides, materials incorporating TITLE OF INVENTION: Polynucleotides for using them. FILE REPERENT 11000.104301. CURRENT APPLICATION NUMBER: US/09/634,238
UNMBER OF SEQ ID NOS: 422
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 220
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US-09-252-991A-26112
; Sequence 26112, Application US/09252991A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 25928, Application US/09252991A patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Lactobacillus rhamnosus US-09-634-238-220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25928
Christensson, Anna C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 TKDKI 126
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-09-252-991A-25928
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APPLICANT: MARC J. RUBERIGED AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: APPLICATION NUMBER: US/09/252, 991A
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-7
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 28143

LENGTH: 1441
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                                                                                                                                                                                                                                                                                                                                                                                                                                              61 SFDLILMDKEMPERDGVSTTKKLREME-----VKSMIVGVTSLADNEEERRAFWEAGLNH 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 LNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERD 75
                                                                                                                                                                                                                                                                                                                                                        2 ATKSMGDIEKIKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAV-IIHRDGGS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76 GVSTTKKLRE....--MEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKII 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.6%; Score 139.5; DB 4; Length 1441; 28.8%; Pred. No. 2.2e-07; Live 30; Mismatches 43; Indels 11;
                                                                                                                                                                                                                                                          Length 1298;
                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                          Query Match 20.6%; Score 139.5; DB 2; Best Local Similarity 31.1%; Pred. No. 1.8e-07; Matches 42; Conservative 28; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 28143, Application US/09252991A Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 220, Application US/09634238 Patent No. 6544772 GENERAL INFORMATION:
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Havukkala, Ilkka J.
Bloksberg, Leonard, N.
Lubbers, Mark W.
Dekker, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Pseudomonas aeruginosa
                                                                                      LENGTH: 1298 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 1298 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 CLAKPLTKDKIIPLI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 28.8%
Matches 34; Conservative
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APPLICANT:
APPLICANT:
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APPLICANT:
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: MARC J.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.13 6
CURENT APPLICATION NUMBER: US 60/074,788
PRIOR PELLING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-07-18
PRIOR FILING DATE: 1998-07-18
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 SFDLILMDKEMPERDGVSTTKKLREM----EVKSMIVGVTSLADNEEERRAFMEAGLNHC 116
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                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

20.0%; Score 135.5; DB 4; Length 860;
Best Local Similarity 26.5%; Pred. No. 3e-07;
Matches 36; Conservative 35; Mismatches 56; Indels 9
                                                                                                                                                                                                                                                                                                                            TYPE: PRT;
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26112
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Search completed: August 13, 2003, 19:13:02 Job time : 18 secs

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August 13, 2003, 19:12:22 ; Search time 54 Seconds (without alignments) 329.934 Million cell updates/sec
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678
1 MATKSMGDIEKIKKKLNVLI......LAKPLTKDKIIPLINQLMDA 136
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/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              492763 segs, 131003257 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000

    protein search,

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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 127, App	Seguence 8, Appli	Sequence 328, App	Sequence 909, App		Sequence 366, App	Sequence 2, Appli	Sequence 7, Appli	Sequence 10049, A	Sequence 4, Appli	Sequence 17, Appl	Seguence 11131, A	Sequence 12532, A	Sequence 9975, Ap	Sequence 13783, A
	ΠD	US-10-101-464A-127	US-09-918-508-8	US-09-801-368-328	US-10-101-464A-909	US-09-801-368-332	US-09-801-368-366	US-10-126-120-2	US-09-918-508-7	US-10-156-761-10049	US-09-424-951-4	US-10-135-322-17	US-09-815-242-11131	US-10-156-761-12532	US-10-156-761-9975	US-09-815-242-13783
	DB	15	10	10	15	10	10	15	10	12	10	14	6	15	15	σ
	Query Match Length DB	261	118	622	1018	1220	712	974	125	1829	1081	2150	227	203	227	232
ďΡ	Query Match	29.8	25.3	22.1	21.5	21.4	21.2	20.3	20.2	19.5	18.9	18.8	18.7	18.6	18.5	18.4
	Score	202	171.5	150	146	145	143.5	137.5	137	132	128	127.5	126.5	126	125.5	124.5
	Result No.		2	e	4	Ŋ	9	7	00	σι	10	11	12	13	14	15

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Sequence 2, Appli Sequence 4, Appli	Sequence 34, Ap	Sequence 12602, A	Sednence 356, App	Sequence 12098, A	Sequence 13746, A	Sequence 11629, A	Sequence 10420, A	Seguence 958, App	Sequence 979, App	Sequence 19, Appl	Sequence 2, Appli	Seguence 13096, A	Sequence 114, App	Sequence 11581, A	Seguence 27, Appl	Sequence 10048, A	Sequence 6370, Ap	Seguence 24, Appl	Sequence 4, Appli	Sequence 30, Appl	Sequence 10, Appl	Sequence 117, App	Sequence 827, App		ednence	Sequence 18, Appl	Sequence 10458, A
-10-116-048-2 -10-116-048-4	US-U9-769-787-54 US-10-156-761-8624	US-10-156-761-12602	US-10-101-464A-956	US-09-815-242-12098	5 US-10-156-761-13746	-09-815-242-11629	US-09-815-242-10420	US-10-101-464A-958	1-464A-979	US-10-135-322-19	US-09-918-508-2	US-10-156-761-13096	US-10-101-464A-114	US-10-156-761-	US-10-100-294	US-10-156-761-	0S-09-138-6	US-09-819-142-	US-09-918-508-4	US-10-135-322-3	US-09-8	US-10-101-464A-11	US-10-101-4	US-10-101-464A-97	US-10-135-322-2	US-10-135-322-18	US-10-156-761
2471	1447	248	1044	248	218	222	232	890	1270	1173	1176	1383	762	243	747	228	235	699	1036	104	573	599	816	1240	100	1092	197
18.3	18.2	18.1	18.1	18.0	17.9	17.8	17.5	17.4	17.4	17.3	17.3	17.3	17.0	16.9	16.7	16.5	16.4	16.4	16.4	16.3	16.2	16.2	16.2	16.2	16.2	16.2	15.8
124	123.5	122.5	122.5	122	121.5	120.5	118.5	118	118	117.5	117.5	117	115	114.5	113	112	111.5	111	111	110.5	110	110	110	110	109.5	109.5	107
16	18 10	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Sequence 127, Application US/10101464A
; Sequence 127, Application US/2030046728A1
; Publication No. US20030046728A1
; GENERAL INFORMATION:
 APPLICANT: Strabala Timothy
; APPLICANT: Micuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
 TITLE OF INVENTION: Compositions Isolated from Plant Cells
 TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
 FILE REFERENCE: 11000.1020c2
 CURRENT APPLICATION NUMBER: US/10/10/1464A
 CURRENT APPLICATION NUMBER: 09/704/302
 PRIOR PILING DATE: 2000-11-01
 PRIOR FILING DATE: 1999-01-12
 PRIOR FILING DATE: 1999-01-12
 PRIOR FILING DATE: 1999-11-01
 PRIOR APPLICATION NUMBER: PCT/US00/00724
 PRIOR APPLICATION NUMBER: PCT/US00/00724
 PRIOR PILING DATE: 1999-11-01
 PRIOR PILING DATE: 1999-11-01
 PRIOR PILING DATE: 1999-11-01
 PRIOR PILING DATE: 1999-11-01
 PRIOR PILING DATE: 1900-01-11 2; 18 VLIVDDDPLNLIIHEXIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV 77 Gaps 78 STTKKLREMEVKSMIVGVISLADNEEERRAFMEAGLNHCLAKPLIKDKIIPLINQ 132 5 Length 261; Indels Query Match
29.8%; Score 202; DB 15;
Best Local Similarity 36.5%; Pred. No. 4.4e-14;
Matches 42; Conservative 34; Mismatches 37; NUMBER OF SEO ID NOS: 989 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 127 Pinus radiata US-10-101-464A-127 US-10-101-464A-127 g δλ

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RESULT 4
US-10-101-464A-909
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TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE PERENEROR: 109272.147
CURRENT APPLICATION NUMBER: US/09/801,368
CURRENT FILING DATE: 2001-03-07
PRIOR PRILING DATE: 2000-01-19
PRIOR FILING DATE: 2000-01-19
PRIOR FILING DATE: US 60/160,587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 VLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 ILVVDDHPINRRLLADQLGSLGYQCKTANDGVDALNVL--SKNHIDIVLSDVNMPNMDGY 63
                                                                                                                                                                                                 APPLICANT: KAKIMOTO, TATSUO
APPLICANT: KAKIMOTO, TATSUO
APPLICANT: HIGGELI, MASAUKI
APPLICANT: HIGGELI, MASAUKI
APPLICANT: HIGGELI, MASAUKI
APPLICANT: INOUE, TSUOMU
TITLE OF INVENTION: ANALYSIS OF AGONIST-ACTIVITY
TITLE OF INVENTION: TO CYTOKININ RECEPTOR
FILE REPERBNE: 065479
CURRENT APPLICATION NUMBER: US/09/918,508
CURRENT FILING DATE: 2001-08-01
PRIOR PAPLICATION NUMBER: UF 2001-03-15
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PALENTIN VET: 2.1
SSQ ID NO 8
LENGTH: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 25.3%; Score 171.5; DB 10; Length 118; Best Local Similarity 33.9%; Pred. No. 3.2e-11; Matches 37; Conservative 32; Mismatches 37; Indels 3; Gaps
78 STIKKLREMEVKSMIVGVISLADNEEERRAFMEAGLNHCLAKPLIKDKI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 RLIQRIRQLGLILPVIGVTANALAEEKQRC-LESGMDSCLSKPVTLDVI 111
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                                                                                                             US-09-918-508-8; Application US/09918508; Sequence 8, Application US/09918508; Patent No. US2002017162A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 440
SOFTWARE: Patentin version 3.0
SEQ ID NO 328
LENGTH: 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT; ORGANISM: Escherichia coli
US-09-918-508-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Busby, Robert
Cali, Brian
APPLICANT: Cali, Petan
APPLICANT: Hecht, Petar
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salama, Sofie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sherman, Amir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maxon, Mary
Milne, Todd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Royer, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Silva, Jeff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-801-368-328
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APPLICANT:
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DP
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| APPLICANT: Strabala, Timothy | APPLICANT: Strabala, Timothy | APPLICANT: Strabala, Timothy | APPLICANT: Strabala, Timothy | APPLICANT: Highlish Colleen W. | APPLICANT: OF INVENTION: Compositions isolated from Plant Cells | APPLICANT: DIONO.10262 | APPLICANT: DIONO.10263 | APPLICANT: DIONO.10264 | APPLICANT: DIONO.10264 | APPLICANT: DIONO.10264 | APPLICANT: DIONO.10266                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (| || : | : | : | : | : | 428 IVMPNLDGATATSIVRSFDNETPIIAMTGNIMN-QDLITYLQHGMNDLLAKPFTRDDLHS 486
                                                                                                                                                                                                                                                                                                                         373 LRKGFHVLLVEDDAVSIQLCSKFLRKYGCTVQVVSDGLSAISTLEKYR----YDLVLMD 427
                                                                                                                                                                                                                                                                                                                                                                                                                                 69 KEMPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKI-- 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               916 DLILMDVCMPVMNGLQATRIIRSFEEMGNWDAAVNAGIELVSSDLSCNGHSSRESKERVP 975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 TKSMGDIEKIKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSF 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             858 SSSIVEEPKPKPKPKILLVEDNKINVMVTQSMMKQLGHSMDVVNNGVEAV--HAVQQSTY
                                                                                                                                                                                                                      12 IKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVII---HRDGGSSFDLILMD
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25.2%; Pred. No. 4e-07;
tive 35; Mismatches 53; Indels 34; Gaps
                                                                                                                    20;
Length 622;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 IVGVISLADNEEERRAFMEAGLNHCLAKPLIKDKIIPLINQLM 134
Ouery Match 22.1%; Score 150; DB 10; Best Local Similarity 28.1%; Pred. No. 7.3e-08; Matches 38; Conservative 32; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence 909, Application US/10101464A publication No. US20030046728A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 332, Application US/09801368 ; Patent No. US20020128250A1 ; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                487 ILIRYLKDRIPLCEQ 501
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ORGANISM: Eucalyptus grandis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 25.28
Matches 41, Conservative
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APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holty Poug
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FESULA 10-126-120-2
Sequence 2, Application US/10126120
Sequence 2, Application US/10126120
Sequence 2, Application Wo. US20030108526A1
SEMENAL INFORMATION:
APPLICANT: SARAKIDARA, Hitoshi
APPLICANT: Takel, Kentan
APPLICANTION: MICRORANISMS FOR USE IN THE MEASUREMENT OF ENVIRONMENTAL FAC
TITLE OF INVENTION WIMBER: US/10/126,120
CURRENT APPLICATION NUMBER: US/10/126,120
CURRENT FILING DATE: 2002-04-19
FRIOR FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 50
SEQ ID NO 2,
SEQ ID NO 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---FMEAG 112
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                                                                                                                                                                                                                                                                                                                                     17 NVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVII----HRDGGSSFDLILMDKEMP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                     .-----MIVGVISLADN 101
                                                                                                                                                                                                                                                                                   10 EKIKKKLNVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDK 69
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Sequence 10520020177162A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: RAINOTO, TATSUO
APPLICANT: HIGUGHI, MASAVIKI
APPLICANT: INOUE, TSUTOMU
APPLICANT: INOUE, TSUTOMU
APPLICANT: INOUE, TSUTOMU
TILLE OF INVENTION: ANALYSIS OF AGONIST-ACTIVITY
TILLE OF INVENTION: TO CYTOKININ RECEPTOR
FILE REPERENCE: 665478
CURRENT FPLICATION NUMBER: US/09/918,508
CURRENT FILING DATE: 2001-08-01
PRIOR FILING DATE: 2001-08-15
PRIOR FILING DATE: 2001-03-15
                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                  31;
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                                                                                                       Query Match
21.2%; Score 143.5; DB 10; Length 712;
Best Local Similarity 27.9%; Pred. No. 4.5e-07;
Matches 39; Conservative 28; Mismatches 42; Indels 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 ERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ::|:| : | | | | ||:
616 MDKRKALL-SGCNDYLIKPV 634
; ORGANISM: Saccharomyces cerevisiae US-09-801-368-366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 EEERRAFMEAGLNHCLAKPL 121
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Best Local Similarity 24.6%
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Zea mays US-10-126-120-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 8
US-09-918-508-7
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TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.11 109272.11 109272.11 109272.11 109272.11 109272.11 109272.11 109272.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 10970.11 1
                                                                                                                                                                                                                                                                 APPLICANT: Sherman, Amir APPLICANT: Sherman, Amir APPLICANT: Silva, Jeff APPLICANT: Silva, Jeff APPLICANT: Summers, Eric TILLE Silva, Jeff TILLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi FILLE REFERENCE: 109272.14 190722.14 190722.14 190722.14 190722.14 190722.14 190722.14 190722.14 190722.14 190722.14 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.10 190722.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 DIEKIKKKLNVLIVDDDPLNLIHEKIIKA---IGGIS--QTANNGEEA---VIIHRDGG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 29.0%; Pred. No. 6.6e-07;
Matches 40; Conservative 40; Mismatches 44; Indels 14
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Milne, Todd
No. US20020128250Alman, Thea
                                                                                                            Milne, Todd
No. US20020128250Alman, Thea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT CRGANISM: Saccharomyces cerevisiae US-09-801-368-332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1195 KPIKRPKLKTILTEFCAA 1212
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SOFTWARE: Patentin version 3.0
SEQ ID NO 366
LENGTH: 712
TYPE: PRT
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APPLICANT: Call, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Revin
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Sherman, Amir
                                                                                                                                                                                                                                      Salama, Sofie
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                                                                   Maxon, Mary
                                                                                                                                                                                         Royer, Johr
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US-09-801-368-366
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US-10-135-322-17
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                                                                                                                                                                                                                                                                                                              68 DKEMPERDGVSTTKKL-REMEVKSMIVGVTSLADNEEERRAFWEAGLNHCLAKPLTKDKI 126
                                                                                                                                                                                                                                                                                                                                      4 VKILVVEDNHVN----QEVIKRMLNLEGIENIELACDGQEAFDKVKELTSKGENYNMIFM 59
                                                                                                                                                                                                                                    16 LNVLIVDDDPLNLITHEKIIKA -- - IGGIS -- QTANNGEEA -- - VIIHRDGGSSFDLILM 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51; Indels 10; Gaps
                                                                                                                                                                                              14; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1829;
                                                                                                                                                      Length 125;
                                                                                                                                                                                              37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 31.5%; Pred. No. 3.1e-05;
Matches 39; Conservative 24; Mismatches 51;
                                                                                                                                                      Ouery Match 20.2%; Score 137; DB 10; Best Local Similarity 29.4%; Pred. No. 2.1e-07; Matches 37; Conservative 38; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: OMURA, SATOSHI
APPLICANT: ISHIRAMA, UND
APPLICANT: SHIRAMA, HROSHI
APPLICANT: SHIRAMA, HROSHI
APPLICANT: SHIRAMA, HROSHI
APPLICANT: SAKAKI, YOSHIVUKI
CURENT APPLICATION NUMBER: US/10/156,761
CURRENT FILIKG DATE:
CURRENT FILIKG DATE:
CURRENT FILIKG DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10049, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Streptomyces avermitilis
US-10-156-761-10049
                                                                                               ORGANISM: Saccharomyces cerevisiae US-09-918-508-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 4, Application US/09424951
; Patent No. US20020137034A1
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2
SEQ ID NO 7
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LENGTH: 1829
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                                                       LENGTH: 125
                                                                              TYPE: PRT
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2024 RKK--ALIVEDNELNRKVLAQLFKKIDWIISFAENGREA-LKEIIGERCFDIVFMDCQMP 2080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 LILMDKEMPERDGVSTTKKLREMEVKS------MIVGVTS---LADNEEERRAFME 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         920 VYLMDVQMPVMGGFBATBKIRQWEKKSNPIDSLTFRTPIIALTAHAMLGDREKS----LA 975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
              APPLICANT: SOLL, DAVID R.

TITLE OF INVENTION: CANDIDA ALBICANS TWO-COMPONENT HYBRID KINASE GENE,
TITLE OF INVENTION: CANTKI, AND USE THEREOF
FILE REFERENCE: 087714/0113
CURRENT APPLICATION NUMBER: US/09/424,951
CURRENT FILING DATE: 1998-06-05
PRIOR FILING DATE: 1998-06-05
PRIOR FILING DATE: 1997-06-06
NUMBER OF SEQ ID MOS: 7
SOFTWARE: PATENTIN VET: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BERNEY, PN
APPLICANT: HELRERIUTTA, Y
APPLICANT: HELRERIUTTA, Y
APPLICANT: HELRERIUTTA, Y
APPLICANT: MAHONEN, AP
APPLICANT: SAUPETINEN, L
APPLICANT: RAUPETINEN, L
APPLICANTON: WOODEN LEG GENE, PROMOTER AND USES THEREOF
FILE REPRENCE: 5014-086-999
CURRENT APPLICATION NUMBER: US/10/135,322
CURRENT FILING DATE: 2002-04-30
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PALENTIN Version 3.0
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Best Local Similarity 32.5%; Pred. No. 0.00012;
Matches 37; Conservative 20; Mismatches 50; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 18.9%; Score 128; DB 10; Length 10 Best Local Similarity 28.3%; Pred. No. 4e-05; Matches 43; Conservative 31; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           976 KGMDDYVSKPLKPKLLMQTIKKCIHNINQLKE 1007
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THYAGARAJAN
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US-10-135-322-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , ORGANISM: Candida albicans US-09-424-951-4
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65 ILMDKEMPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKD 124
                                                                                                                                                                                                                                                                                                                                                                                                                           75 DGVSTTKKLREMEVKSMIVGVISLAD-------NEBERRAFMEAGLNHCLA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 EKIKKKLNVLIVDDDPLNLIHEKIIKAIG---GIS--QTANNGEEAVIIHRDGGSSFDL 64
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                                                                                                                                                                                                                                                                              20;
                                                                                                                                                                                                                              Length 203;
                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                            Query Match
18.6%; Score 126; DB 15;
Best Local Similarity 29.5%; Pred. No. 6.5e-06;
Matches 36; Conservative 20; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Squence 9975, pplication US/10156761
Squence 9975, pplication US/2003019018A1
GENERAL INPORMATION:
APPLICANT: OMORA, SATOSHI
APPLICANT: SHIKAWA, JUN
APPLICANT: HSHIKAWA, JUN
APPLICANT: HSHIKAWA, HON
APPLICANT: HSHIKAWA, HON
APPLICANT: HATTORI, MASHIRA
APPLICANT: HATTORI, MASHIRA
APPLICANT: HATTORI, MASHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-26
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PELICATION NUMBER: JP 2001-272697
PRIOR PELICATION NUMBER: JP 2001-272697
NUMBER OF SEQ ID NOS: 15109
SSC ID NO 9975
LENGTH: 227
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ 1D NOS: 15109
SEQ ID NO 12532
LENGTH: 203
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US-09-815-242-13783
; Sequence 13783, Application US/09815242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Streptomyces avermitilis US-10-156-761-9975
                                                                                                                                                    ORGANISM: Streptomyces avermitilis US-10-156-761-12532
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                                                                                                                                                                                                                                                                      APPLICANT: Wall, Daniel
APPLICANT: Tradick, John D.
APPLICANT: Tradick, John D.
APPLICANT: Yamancho, Robert T.
APPLICANT: Yamancho, Robert T.
APPLICANT: Yamancho, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: DATE: 2001-03-21
CURRENT FILING DATE: 2001-03-21
PRIOR PPLICATION NUMBER: 60/296,848
PRIOR FILING DATE: 2000-03-21
PRIOR PPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PLILING DATE: 2000-05-26
PRIOR PLILING DATE: 2000-10-23
PRIOR PLILING DATE: 2000-10-23
PRIOR PLILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/265,931
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-11-27
PRIOR PLILING DATE: 2000-12-22
PRIOR PLILING DATE: 2000-12-22
PRIOR PLILING DATE: 2001-02-16
NUMBER OF SED ID NOS: 14110
SOFTWARE: FESTSEQ for Windows Version 4.0
SED ID NO 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
18.7%; Score 126.5; DB 9;
Best Local Similarity 29.1%; Pred. No. 6.7e-06;
Matches 34; Conservative 30; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SQUENCE 12332, Application US/10156761
PUBLICATION NO. US20030119018A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIRAWA, HIROSHI
APPLICANT: SHIRAW, HIROSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, WASAHIRA
TILLE OR INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
FRIOR FILING DATE: 2001-204089
                                                                                                          Sequence 11131, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Haemophilus influenzae US-09-815-242-11131
                                                                                                                                                                                                            Ohlsen, Kari E.
Zyskind, Judith W.
Wall, Daniel
                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 13
US-10-156-761-12532
                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
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a ò d

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18.4%; Score 124.5; DB 9; Length 232; 28.2%; Pred. No. 1.1e-05; tive 31; Mismatches 48; Indels 5;
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Haselbeck, Rabit. L.
APPLICANT: Obleson, Rail. L.
APPLICANT: Systind, Judith W.
APPLICANT: Trandtk, John D.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential
FILE REPERBNCE: ELITRA.011A
CURRENT APPLICATION NUMBER: 60/13,078
FRIOR PLILING DATE: 2000-03-21
CURRENT FILING DATE: 2000-05-23
FRIOR FILING DATE: 2000-05-23
FRIOR PLICATION NUMBER: 60/207,727
FRIOR PLICATION NUMBER: 60/207,727
FRIOR PLILING DATE: 2000-05-23
FRIOR PLILIATION NUMBER: 60/207,727
FRIOR PLILIATION NUMBER: 60/257,931
FRIOR PLILIATION NUMBER: 60/253,625
FRIOR PLILIATION NUMBER: 60/257,931
FRIOR PLILIATION NUMBER: 60/257,931
FRIOR PLILIATION NUMBER: 60/257,931
FRIOR FILING DATE: 2000-12-22
FRIOR APPLICATION NUMBER: 60/253,625
FRIOR FILING DATE: 2000-12-22
FRIOR FILING DATE: 2000-12-22
FRIOR FILING DATE: 2000-13-36
FRIOR FILING DATE: 2001-03-16
FRIOR FILING DATE: 2001-13-16
FRIOR FILING DATE: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Salmonella typhi
US-09-815-242-13783
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:|:|||| : ::::: | | |::||:|: | | ||::||: | 4 ILLVDDDRELTSLLKELLEMEGENVLVAHDGEQALELLDD---SIDLLLLDVMMPKKNGI 60 18 VLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV 77 78 STTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLINOLM 134 Query Match
Best Local Similarity 28.2%
Matches 33; Conservative οy g Óγ

Search completed: August 13, 2003, 19:20:55 Job time : 55 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

August 13, 2003, 19:09:57; Search time 19 Seconds (without alignments) 688.365 Million cell updates/sec Run on:

Title:

US-09-646-679-15 678 1 MATKSMGDIEKIKKKLNVLI......LAKPLTKDKIIPLINQLMDA 136 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	histidine kinase h	rotein e		sensor f	sensor histidine k	sensor protein Rcs	prote	t	hypothetical prote	two component sens	sensory box histid	aerobic respiratio	response regulator	sensor histidine k.	nt hyb	× T	protei	sensory box histid	response regulator	sensor histidine k	sensory box histid	Ψ	axi	hist		sensory transducti	aerobic mespinatio	sen	cell wall assembly
SUMMARIES	ID	T08875	G65010	A91035	C85879	H87640	AD0790	BVECCC	C91017	E85861	AD0149	E87644	AD0432	A69487	C82151	AG1897	B87252	A35966	A87580	G69422	E82198	A87617	S58645	G84253	A87266	S75023	S75525	AG0906	AB0032	A49344
	DB	7	٦	7	(1	7	7	Н	N	N	N	(7	C/I	Ŋ	Ŋ	C)	~	7	~	7	7	7	Н	~	7	Н	7	7	N	Н
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ď	Quer	7	Ñ	Ñ	Ñ۱	7	7	7	Ċ	C)	Cή	Ċ	Ċ	2	C)	N	7	7	C)	(7)	71	7	C	7	(1)	7	CI	7	CI	7
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probable sensor/re	aerobic respiratio	aerobic respiratio	aerobic respiratio	sensor/response re	probable two-compo	SLN1 protein - yea	sensor histidine k	sensor histidine k	probable sensor/re	SSK1 protein - yea	sensor histidine k	sensory box histid	sensor protein (im	probable response	two-component regu
A83324	RGECAR	A91140	D85985	E83529	F83153	S48387	E87460	C82424	E83212	S64828	C87575	D87559	AI0860	H97516	B41863
7		C)	N	N	7	7	7	7	7	7	7	7	N	N	N
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22	22	22	22	21	21	21	21	21	21	21	21	21	21	20	20
150	149.5	149.5	149.5	148	147	145	144.5	144	144	143.5	143	142.5	142,5	142	142
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	4 5

ALIGNMENTS

PRESULT 1 N. Alteriane Atlane promotor DHKB - sline mold (Dictyostellum discoldeum) N. Alteriane Atlane Public distillation through the property of the promotor of the promotor of the profit of the promotor of the promotor of the profit o	Science 277, 1453-1462, 1997 A.Title: The complete genome sequence of Escherichia coll K-12. A.Reference number: A64720; MUID:97426617; PMID:9278503
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Subsort histidine kinase/response regulator [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001
C;Accession: H87640
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, T.T.; Nelson, K.E.; Eisen, J.; Heidelberg,
B;Jabb, M.T.; DeBooy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Ko
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Pieference number: A87249; MuID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1013 PNVDGFELTRKLREQNSSLPINGLTANA-QANEREKGLNCGMNLCLFKPLTLDVLKTHLS 1071
                                          72 PERDGYSTTKKLREMEVKSMIVGYTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLIN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Cross-references: GB: AE005673; NID: 913424832; PIDN: AAK25124.1; GSPDB: GN00148
                                                                                                                                        72 PERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLIN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 955 LPEKLSILIADDHPTNRLLIKRQINLIGYDVDEATDGVQA--LHKVSMQHYDLLITDVNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 IKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEM
12 IKKKLNVLIVDDDPLNLIIHEKIIKAIGGISOTANNGEEAVIIHRDGGSSFDLILMDKEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: evgS
C;Superfamily: evgS protein; response regulator homology
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34.4%; Pred. No. 7.5e
:ive 25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25.7%; · Score 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 26.0%
Best Local Similarity 34.4%
Matches 42; Conservative
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                                                                                                                                                                                                                                                                                            132 QL 133
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A;Gene: CC3162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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H87640
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A91035
Probable sensor for regulator EvgA [imported] - Escherichia coli (strain O157:H7, substr C; Species: Bscherichia coli
C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 24-Aug-2001
C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 24-Aug-2001
C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 24-Aug-2001
C; Date: 18-Jul-2001
R; Hayashi, T: Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
By Hayashi, T: Nakino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gency A; Escension: A91035
A; Status: preliminary
A; Molecule type: DNA
A; Status: preliminary
A; Molecule type: DNA
A; Status: 1-197 <-HMX>
A; Status: 1-1197 <-HMX>
A; Status: 1-1197 <-HMX>
A; Cross-references: GB:BA000007; PIDN:BAB36672.1; PID:g13362719; GSPDB:GN00154
A; Experimental source: strain 0157:H7, substrain RIMD 050952
                                                                                                                                                                                                                                 A.Description: Wavely dentified genes involved in signal transduction of Escherichia col A.Reference number: J0020

A.Reference number: J0021

A.Accession: J0021

A.Accession: J0021

A.Residues: 1-151, F', 153-241, PL', 244-274, R', 276-419, FE', 422-738, D', 740-757, K', 759-8705 and 140, 73-77, 1994

A.Title: Newly identified genes involved in the signal transduction of Escherichia coli A.Accession: 14120

A.Accession: 14120

A.Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A. Molecule Type: DNA
A. Residues: 1-151, Fr. 153-241, PL', 244-274, R', 276-419, FE', 422-738, 'D', 740-757, K', 759-
A. Cross-references: GB:D14008; NID:9456162; PIDN:BAA03108.1; PID:9216554
C. Genetics:
C. Genetics:
C. Superfamily: evgS protein; response regulator homology
C. Reywords: autophosphorylation; phosphohistidine; phosphoprotein; phosphotransferase; the St. 935-fonanin; sensor histidine kinase homology SHRA-
F: 867-935-fonanin; sensors regulator homology SHRA-
F: 961-1070-fonanin; response regulator homology SHRA-
F: 961-1070-fonanin; response regulator homology RRHA-
F: 721/Binding site: phosphate (His) (covalent) #status predicted
F: 1009/Binding site: phosphate (Asp) (covalent) #status predicted
                                                                             A;Residues: 11197 - CBLAT>
A;Residues: 11197 - CBLAT>
A;Cross-references: GB:AE000325; GB:U00096; NID:g1788709; PIDN:AAC75429.1; PID:g1788713;
A;Experimental source: strain K-12; substrain MG1655
R;Utsumi, R:Utsumi, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LPEKLSILIADDHPINRLLLKRQLNLLGYDVDEATDGVQA--LHKVSMQHYDLLITDVNM 1012
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m
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   nucleic acid sequence not shown; translation not shown a type: DNA
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C;Superfamily: evgS protein; response regulator homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26.3%; Score 178.5; DB 1; 34.4%; Pred. No. 5.1e-07; tive 25; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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es 42; Conserv
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Best Local Similarity
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sensor for ctr capsule biosynthesis [imported] - Escherichia coli (strain 0157:H7, su cispecies: Escherichia coli (cjatei 18-011-2001 #sequence_revision 18-011-2001 #text_change 03-Aug-2001 C;Accession: C91017 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C;Accession: C91017 R; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res 8, 11-22, 2001 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and characteric complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and characteric control of the con
A;Title: RosB and RosC: a two-component regulator of capsule synthesis in Escherichii A;Reference number: JV0068; MUID:90130299; PMID:2404948
A;Accession: JV0069
A;Accession: JV0069
A;Rolecule type: DA
A;Residues: 1-112, IG', 115-918, 'S', 920-933 <STO>
A;Residues: 1-112, IG', 115-918, 'S', 920-933 <STO>
A;Cross-references: GB:M28242; NID:g147524; PIDN:AAA24503.1; PID:g147525
A;Experimental source: strain K12
                                                                                                                                                                                                                                                                                              A,Gene: rosc.
A,Gene: rosc.
A,Gene: rosc.
C,Superfamily: rosc protein; response regulator homology
C,Superfamily: rosc protein; capsule synthesis; phosphohistidine; phosphoprotein,
C,Kewyords: autophosphorylation; capsule synthesis; phosphohistidine; phosphoprotein,
E,4-26/Domain: transmembrane #status predicted <TM1>
F,298-318/Domain: transmembrane #status predicted <TM2>
F,319-310/Domain: response regulator homology <ARN>
E,463/Binding site: phosphate (His) (covalent) #status predicted
F,859/Binding site: phosphate (Asp) (covalent) #status predicted
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A;Residues: 1-933 «HAIX>
A;Cross-references: GBA000007; PIDN:BAB36530.1; PID:913362576; GSPDB:GN00154
A;Experimental source: strain 0157:H7; substrain RIMD 0509952
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hes 37; Conservative
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Best Local Si
Matches 37;
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N.Alternate names: regulatory protein rcsC
C.Species: Escherichia coli
C.Species: Escherichia coli
C.Species: Escherichia coli
C.Species: Ascherichia coli
C.Species: Allore 1991 #sequence_revision 17-Oct-1997 #text_change 01-Mar-2002
C.Accession: H64991; JV0069; A48659
C.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A.Title: The complete genome sequence of Escherichia coli K-12.
A.Reference number: A64720; MuID:97426617; PMID:9278503
A.Accession: H64991
A.Scatus: preliminary; nucleic acid sequence not shown; translation not shown
A.Molecule type: DNA
A.Residues: 1-933 CBLAT>
A.Cross-references: GB.AE00311; GB:U00096; NID:91788547; PIDN:AAC75278.1; PID:91788548;
A.Experimental source: strain K-12, substrain MG1655
A.Sctot, V.; Gottesman, S.
J. Bacteriol. 172, 659-669, 1990
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A;Residues: 1-948 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD07502.1; PID:g16503497; GSPDB:GN00176
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                                                                                                                                                        14 KKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPE
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                                                                     Indels
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C;Superfamily: rcsC protein; response regulator homology
C;Keywords: phosphotransferase
                                                                     49;
                       ed. No. 3.4e-07;
Mismatches 49
                                Pred. No.
                                                                          31;
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hes 37; Conservative
                  Best Local Similarity 31.7% Matches 39; Conservative
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A; Status: preliminary
A; Molecule type: DNA
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Article: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7.
A.; Reference number: A65480; MUD:21074935; PMID:11206551
A.; Accession: E85861
A.; Accession: E85861
A.; Status: preliminary
A.; Molecule type: DNA
A.; Molecule type: DNA
A.; Molecule type: DNA
A.; Residences: GB:AE005174; NID:q12516556; PIDN:AA657353.1; GSPDB:GN00145; UWGP:Z34
A.; Experimental source: strain 0157:H7, substrain EDL933
C.; Genetics:
A.; Ge
                                                                                                                                            hypothetical protein rcsC [imported] - Escherichia coli (strain 0157:H7, substrain EDL93 C; Species: Escherichia coli coli coli coli escherichia coli escherichia coli sequence_revision 16-Feb-2001 #text_change 14-Sep-2001 C; Accession: E85861 R; Accession: E85861 R; Plunkett III, G; Burland, V; Mau, B; Glasner, J.D.; Rose, D.J.; Mayhew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  two component sensor kinase/response regulator protein RcsC (EC 2.7.3.-) [imported]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 LNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERD 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 VLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RLIQRIRQLGLTLPVIGVTANALAEEKQRC-LESGMDSCLSKPVTLDVI 916
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25.3%; Score 171.5; DB 2; Length 933; 33.9%; Pred. No. 1.5e-06; Live 32; Mismatches 37; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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C;Superfamily: rcsC protein; response regulator homology
C;Keywords: phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 25.3%; Score 171.5; DB 2; Best Local Similarity 35.1%; Pred. No. 1.5e-06; Matches 39; Conservative 29; Mismatches 40;
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Best Local Similarity
Matches 37; Conserv
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C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C;Accession: Ab0432
C;Accession: Ab0432
Aparkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G. 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: Ab0001; MUID:21470413; PMID:11586360
sensory box histidine kinase/response regulator [imported] - Caulobacter crescentus C; Species: Caulobacter crescentus C; Species: 20-Apr-2001 (c) Date: 2
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C;Superfamily: aerobic respiration control sensor protein arcB; response regulator ho
C;Keywords: phosphotransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Status: preliminary
A, Modecule type: DNA
A, Residues: 1-642 <58TO>
A, Cross-references: GB:ABOO5673; NID:913424865; PIDN:AAK25153.1; GSPDB:GN00148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 LNVLIVDDDPINLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERD
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24.0%; Score 162.5; DB 2;
Best Local Similarity 27.0%; Pred. No. 6.8e-06;
Matches 33; Conservative 38; Mismatches 48;
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24.0%; Score 162.5; DB 2;
Best Local Similarity 33.0%; Pred. No. 5.5e-06;
Matches 36; Conservative 28; Mismatches 40;
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Search completed: August 13, 2003, 19:12:39 Job time : 20 secs
                                                         706 PIAEHELDMALEQ 718
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Best Local Similarity
Matches 39; Conservat
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response regulator homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Daccession: A69487
C;Accession: A69487
E;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
J; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, B.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
Smith, H.O.; Woese, C.R.; Venter, J.S.
Smith, H.O.; Woese, C.R.; Venter, J. Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Residues: 1-17 CKLE>
A;Residues: 1-17 CKLE>
A;Residues: 1-17 CKLE>
A;Residues: 1-17 CKLE>
A;Cross-references: GB:AE000971; GB:AE000782; NID:92689294; PIDN:AAB89351.1; PID:9264864
C;Superfamily: signal transduction receiver (phosphoacceptor) protein (CheY-like); respective (phosphoatein) response regulator homology CRRE>
F;50/Binding site: phosphate (Asp) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sensor histidine kinase VC1831 [imported] - Vibric cholerae (strain N16961 serogroup Ol) C; Species: Vibrio cholerae (C. Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C; Accession: 08151 R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeway, M.D.; Vanathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F Nature 406, 477-483, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Nolecule type: DNA.
A;Residues: 1-736 <HEL>
A;Residues: 1-736 <HEL>
A;Cross-references: GB:AE004259; GB:AE003852; NID:g9656353; PIDN:AAF94979.1; GSPDB:GN001
A;Experimental source: serogroup Ol; strain NI6961; biotype El Tor
C;Genetics:
A;Gene: VC1831
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A;Areference number: A82035; MUID:20406833; PMID:10952301
A;Accession: C82151
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 EMPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDXIIPL 129
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Best Local Similarity 28.3%
Matches 36; Conservative
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C.Species: Nostoc sp. PCC 7120
A,Note: Nostoc sp. PCC 7120
A,Note: Nostoc sp. PCC 7120
C.Species: Nostoc sp. PCC 7120
A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A,Reference number: AB1807; MUID:21595285; PMID:11759840
A,Accession: AG1897
A,Accession: AG1897
A,Residues: 1-1645 KUR>
A,Rolecule type: DNA
A,Residues: 1-1645 KUR>
A,Cross references: GB:BA000019; PIDN:BAB72686.1; PID:g17130074; GSPDB:GN00179
A,Experimental source: strain PCC 7120
C.Senetics:
A,Genetics:
A,Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 TKSMGDIEKIKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.5%; Score 159; DB 2; L4 27.7%; Pred. No. 3.1e-05; tive 40; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1531 DDLINKPFSEKEILEKLNKYL 1551
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PLTKDKIIPLINQ 132
120
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Page 1

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

August 13, 2003, 19:08:31; Search time 11 Seconds (without alignments) 581.421 Million cell updates/sec Run on:

US-09-646-679-15 678 1 MATKSMGDIEKIKKKLNVLI......LAKPLTKDKIIPLINQLMDA 136 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

127863 segs, 47026705 residues Searched: 127863 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_41:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

scription	escherichia		salmonell			myxococcus		escherichia	escherichia	(A)	g	pseudomonas	bacillus	bacillus ha		bordetell			plectonem	shigella	vibrio harv	salmonell	salmonell		vibrio	schizosac		haemophilus		+1	schizosacch	a	pseudomonas
Descri	P30855	P58402	056128	P58662	P14376	P18769	P38889	P58363	P22763	P39928	007084	P48027	P96602	09k998	P24072	P16575	P39486	P26607	P51586	P59342	P54302	Q8z333	P25852	P40330	P54301	P87323	P26762	P44895	09abd9	P96126	014283	P14375	P26275
n	* 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1																																
SUMMAKIES ID	EVGS_ECOLI	EVGS_ECO57	RCSC_SALTI	RCSC_SALTY	RCSC_ECOLI	FRZE_MYXXA	SKN7_YEAST	ARCB_ECO57	ARCB_ECOLI	SLN1_YEAST	SSK1_YEAST	GACS_PSESY	DCTR_BACSU	DCTR_BACHD	CHEY_BACSU	BVGS_BORPE	DCTR_BACME	BARA_ECOLI	YSO1_PLEBO	BARA_SHIFL	LUXQ_VIBHA	ZRAR_SALTI	ZRAR_SALTY	BVGS_BORPA	LUXN_VIBHA	MCS4_SCHPO	BVGS_BORBR	CPXR_HAEIN	- 1	CHEY_TREPA	SCHP	မ	ALGR_PSEAE
DB		H	-4	Н	н	-	Н	~4	-	_	7										-	Н	٦	~	7	-	-	-	-	1	r-d	rH	7
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ry	1 10	10	in	IO	10	m	\sim	\sim	$^{\circ}$	~	_	\circ	0	\circ	σ	g,	19.7	on	σ	σ	σ	σ	σ	σ	g,	æ	യ	œ	œ	œ	18.3	18.1	18.0
Score	:	76.	73.	ä	71.	56.	150	σ.	49.	7	•	マ	40.	40.			33.		32.	32.			31.			27.			25.			122.5	
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Q8x613 escherichia P10957 escherichia O34534 bacilos su Q45994 caulobacter P1624 escherichia Q4406 alcaligenes P49246 xanthomonas Q56312 thermotoga P51358 porphyra pu P43501 pseudomonas Q06065 escherichia O78428 guillardia
ZRAR_ECO57 NARL_ECOLI CITT_BACSU CITRA_CAUGR CPXR_ECOLI CZCR_ALCEU CZCR_ALCEU CZCR_ALCEU CZCR_ALCEU ZYCZT_PORPU PILL_PERABA PILL_PERABA ATOC_ECOLI YCZT_GUITH
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2441 2216 2231 2231 2231 244 2611 2611 2611
117.6 117.6 117.6 117.0 117.0 116.6
121.5 1119.5 1119.5 1119.5 1117 1115.5 1112.5 1112.5
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## ALIGNMENTS

RESULT 1  EVGS_EOCL  EVGS_EOCL  DJ 01-001  DJ 1-001  DJ 1-001  DD 28-FFE  GN ESCHE  COC EDICECT
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As Oshims I. Oyama S. Saito N., Sampel C., Satoh Y., Sivasundaram S., Argami. H. Tahahahil E., Takkad J., Takenoov C., Marenoov C., Takenoov C., Tak
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72 PERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLIN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 IKKKLNVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEM 71
                                                            125/ PHOSPHORIATION (AUTO-) (BY SIMILARITY).
1009 PHOSPHORIATION (BY SIMILARITY).
1137 PHOSPHORIATION (BY SIMILARITY).
1137 F-> S (IN EVGS1; CONSTITUTIVELY ACTIVE).
152 F-> G (IN EVGS1; CONSTITUTIVELY ACTIVE).
152 F-> P (IN REF. 1 AND 2).
153 F-> P (IN REF. 1 AND 2).
154 F-> P (IN REF. 1 AND 2).
155 SQ -> FE (IN REF. 1 AND 2).
156 G-> F (IN REF. 1 AND 2).
157 SQ -> P (IN REF. 1 AND 2).
158 G-> P (IN REF. 1 AND 2).
159 G-> P (IN REF. 1 AND 2).
161 C-> V (IN REF. 1 AND 2).
162 F-> P (IN REF. 1 AND 2).
163 F-> P (IN REF. 1 AND 2).
164 F-> P (IN REF. 1 AND 2).
165 F-> P (IN REF. 1 AND 2).
165 F-> P (IN REF. 1 AND 2).
167 S-> L (IN REF. 1 AND 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRIN-0157:H7 / KIND 0509952;
MEDLINE-21156231; PubMed=11258796;
MEDLINE-21156231; PubMed=11258796;
MEDLINE-21156231; PubMed=11258796;
Hayashi T., Makino K., Ohlsüni M., Murata T., Tanaka M., Tobe T.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
Kunnera S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1] SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDILINE=21074935; Pubmed=11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Perna N.T., Plunkett G. III, Burland V., Mau C., Kirkpatrick H.A.,
Rose D.J., Mayhew G.P., Evans P.S., Gregor J., Kirkpatrick H.A.,
Rose D.J., Mayhew G.P., Evans P.S., Gregor J., Kirkpatrick H.A.,
Grocheck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Amelon R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NOBI_TAXID-83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 1197;
                                                                                                                                                                                                                                                                                                                                                                                                                                     52; Indels
CYTOPLASMIC (POTENTIAL)
                  HISTIDINE KINASE,
RESPONSE REGULATORY.
                                                                                                                                                                                                                                                                                                                                                                                           26.3%; Score 178.5; DB 34.4%; Pred. No. 2.9e-07; ive 25; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Sensor protein evgS precursor (EC 2.7.3.-).
EvgS or 23632 OR ECS3249.
                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 34.4
nes 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
  1197
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11034
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11037
1521
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1523
704
701
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                                                          DOMAIN
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MOD_RES
MOD_RES
VARIANT
                                                                                                                                                                                           CONFLICT
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                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
            system evgS/evgA.
in response to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
MW; A01055089D9618E2 CRC64;
                                                                                ij
Res. 8:11-22(2001).
FUNCTION: Member of the two-component regulatory system evgS/evg Phosphorylates evgA via a four-step phosphorelay in response to environmental signals (By similarity).
SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                      Length 1197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sensory transduction, Transferase, Kinase, Phosphorylation, Transmembrane, Inner membrane, Signal, Complete proteome. SIGNAL 1 21 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PERIPLASMIC (POTENTIAL).
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RESPONSE REGULATORY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 176.5; DB 1;
Pred. No. 4.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SENSOR PROTEIN EVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Interpro; IPR003594; Arpbind_Arpase.
Interpro; IPR004358; Bact_sens_pr_C.
Interpro; IPR004361; His_kina.
Interpro; IPR005467; His_kinase.
Interpro; IPR005570; Hpt.
Interpro; IPR001789; Response_reg.
Interpro; IPR001311; SBP_glu_receptor.
Interpro; IPR001311; SBP_glu_receptor.
Interpro; IPR001311; SBP_glu_receptor.
Interpro; IPR001312; Harpase_c; 1.
Pfam; PF00512; Harpase_c; 1.
Pfam; PF001312; Harpase_reg.
Pfam; PF001312; Harpase_reg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
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                                                                                                                                                                                                                                                           EMBL; AE005468; AAG57495.1; -.
                                                                                                                                                                                                                                                                        EMBL; AP002561; BAB36672.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26.0%;
34.4%;
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Best Local Similarity
                                                                                                                                                                                                                                                                                  PIR; A91035; A9103
PIR; C85879; C8587
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TRANSMEM
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TRANSMEM
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MOD_RES
SEQUENCE
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  DNA
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12 IKKKLNVLIVDDDPLNLITHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEM 71

'n

3; Gaps

52; Indels

25; Mismatches

Conservative

42;

Matches

8 ò

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                                        1013 PNVDGFELTRKLREQNSSLPIWGLTANA-QANEREKGLNCGMNLCLFKPLTLDVLKTHLS 1071
72 PERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLIN 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [2] SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEGUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN=Ty2 / AICC 700931; MEDLINE-22531367; PubMed=12644504; MEDLINE-22531367; PubMed=12644504; MEDLINE-22531367; PubMed=1264504; Mayhew G.F., Rose D.J., Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J., Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J., Schwartz D.C., Blattner F.R.; "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CI18."; and CI18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -! PTM: Activation probably requires a transfer of a phosphate group between a His in the transmitter domain and an Asp of the receiver domain (By similarity).
-! SIMILARITY: Contains 1 histidine kinase domain.
-! SIMILARITY: Contains 1 PAS (PER-ARNI-SIM) dimerization domain.
-! SIMILARITY: Contains 1 response regulatory domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthesis.";
J. Bacteriol. 178:1691-1698(1996).
J. Bacteriol. 178:1691-1698(1996).
-I- FUNCTION: Member of the two-component regulatory system rcsC/rcsB involved in the regulation of the expression of genes involved in colarity acid capsule synthesis. RcsC probably functions as a membrane associated protein kinase that phosphorylates rcsB in response to environmental signals.
-: SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-21534947; PubMed=11677608; Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Banter S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davies R.M., Dowd L., White N., Farrar J., Cronin A., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamilin N., Haque A., Hien T.T., Holroyd S., Jagels K., Kroph A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Whitehead S., Barrell B.G.; Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; anultiple drug resistant Salmonella enterica serovar Typhi CT18"; Mature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Virlogeux I., Waxin H., Ecobichon C., Lee J.O., Popoff M.Y.; "Characterization of the rcsA and rcsB genes from Salmonella typhi: rcsB through tviA is involved in regulation of Vi antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Sensor protein resC (EC 2.7.3.-) (Capsular synthesis regulator
                                                                                                                                                                                                                                                     948 AA.
                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=TY2 / ATCC 700931;
MEDLINE=96198173; Pubmed=8626298;
                                                                                                                                                                                                                                                                                                                                                                                                       RCSC OR STY2496 OR T0594.
Salmonella typhi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROM N.A.
                                                                                                                                    1072 QL 1073
                                                                                           132 QL 133
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                                                                                                                                                                                                                                                                                                                                                                                    component C)
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056128;
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us-09-646-679-15_1.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 VLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                      RESPONSE REGULATORY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
V; AE3A21701265A865 CRC64;
                                                                                                                                                                                                                                                                             SWART; SM00448; KEC; ...
PROSITE; PS50109; HIS.KIN; 1.
PROSITE; PS50110; PAS: FALSE_NEG.
PROSITE; PS50110; RESPONSE_REGULATORY; 1.
Sensory transduction; Transferase; Kinase; Bacterial capsule;
Inner membrane; Transmembrane; Phosphorylation; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ω
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 SITKKLREMEVKSMIVGVISLADNEEERRAFMEAGLNHCLAKPLIKDKI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                           PERIPLASMIC (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25.6%; Score 173.5; DB 1; 33.9%; Pred. No. 5.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                 PAS.
HISTIDINE KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       948 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33; Mismatches
                                                                                                                Interpro; IPR003594; ATPbind_ATPBase.
Interpro; IPR004358; Bact_sens_pr_C.
Interpro; IPR004358; Bact_sens_pr_C.
Interpro; IPR003661; His_Kina.
Interpro; IPR000641; PAS_domain.
Interpro; IPR001789; Response_reg.
Pfam; PF00512; HisRA; I.
Pfam; PF00512; HisRA; I.
Probom; PF000039; Response_reg; I.
PRINTS; PR00344; BCTRLEENSOR.
Probom; PD000039; Response_reg; I.
SMART; SM00387; HATPASS_C; I.
SMART; SM00388; HisRA; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106237 MW;
                                                                     EMBL; AL627274; CAD07502.1; -. EMBL; AB016836; AA068299.1; -. EMBL; X87809; CAA61095.1; -. HSSP; P06143; 1UDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 33.99
Matches 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            948 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RCSC_SALTY
P58662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOD_RES
MOD_RES
SEQUENCE
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TRANSMEM
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(Probable).
--- PTM: Activation probably requires a transfer of a phosphate group between a His in the transmitter domain and an Asp of the receiver domain (By similarity).
--- SIMILARITY: Contains 1 histidine kinase domain.
--- SIMILARITY: Contains 1 PAS (PER-ARMT-SIM) dimerization domain.
--- SIMILARITY: Contains 1 PAS (PER-ARMT-SIM) dimerization domain.

Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.; "Complete genome sequence of Salmonella enterica serovar Typhimurium LT2.";

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18 VLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV
                                                                                                                                                                                                                                                                                                                                                                       N40 RESPONSE REGULATORY.
179 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
106279 MW; BAAD8DA557D5868B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     3;
                                                                                                                                                                                                                                                                                                                                                                                                       25.4%; Score 172.5; DB 1; Length 948; 34.6%; Pred. No. 7.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 STTKKLREMEVKSMIVGVTSLADNEBERRAFMEAGLNHCLAKPLIKD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     35;
                                                                                                                                                                                                                                                                                                                                                                                                                     32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            948 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
DOMAIN
MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-LIZ / SGSC1412 / ATCC 700720;
MEDLINE-21534948; Pubmed-11677609;
MCCLelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreiffe'p';
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
```

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella.

Salmonella typhimurium.

NCBI_TaxID=602

component C). RCSC OR STM2271.

28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Sensor protein rcsC (EC 2.7.3.-) (Capsular synthesis regulator

STANDARD;

SMART; SM00448; NCC, SMOSTER SMOSTER PSSOIDS; PSSOIDS; PSSOIDS; PSSOIDS; PALSE_NEG.
PROSTIE; PSSOILO; PAS; FALSE_NEG.
PROSTIE; PSSOILO; RESPONSE_REGULATORY; 1.
Sensory transduction; Transferase; Kinase; Bacterial capsule;
Sensory transmembrane; Phosphorylation; Complete proteome.
CYTOPLASMIC (POTENTIAL).

SMART; SM00387; HATPASe_c; 1. SMART; SM00388; HisKA; 1. SMART; SM00448; REC; 1.

STYGENE DESCRIPTION OF STYGENE DESCRIPTION OF STYGENE DESCRIPTION OF STYGENE DESCRIPTION OF STYGENE DESCRIPTION OF STYGENE DESCRIPTION OF STYGENE OF STYGENE DESCRIPTION OF STYGENE OF STYG

EMBL; AE008801; AAL21172.1; -.

StyGene; SG????; rcsC

POTENTIAL.
PERIPLASMIC (POTENTIAL). POTENTIAL. CYTOPLASMIC (POTENTIAL).

DOMAIN TRANSMEM

OMAIN

HISTIDINE KINASE.

77

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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37;
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TRANSMEM
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TRANSMEM
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CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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VARIANT
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Dp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A Kaaai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Mixi T., A Kaai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Mixi T., A Macobuchi K., Mori H., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., A Mashimoto H., Nishio Y., Oshima T., Santo N., Sanpei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Wada C., Tamannto Y., Moliuchi T., A Yamannto Y., Moliuchi T., Takeda J., Takemoto K., Wada C., Tamannto Y., Moliuchi T., T., Takeda J., Takemoto K., Wada C., Tamannto Y., Manannto T., Takeda J., Takemoto K., Wada C., Takemoto Y., Moliuchi T., Takeda J., Takemoto K., Wada C., Takemoto Y., Moliuchi T., Takeda J., Takemoto K., Wada C., Takemoto T., DNA Sequence of the You-component regulatory system rcsC/rcsB C. FUNCTION: Member of the two-component regulatory system rcsC/rcsB C. Involved in the regulation of the expression of genes involved in response to environmental signals.

C. -: SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i. PTM: Activation probably requires a transfer of a phosphate group between a His in the transmitter domain and an Asp of the receiver domain (By similarity).
-i. SIMILARITY: Contains I histidine kinase domain.
-i. SIMILARITY: Contains I PAS (PER-ARNT-SIM) dimerization domain.
-i. SIMILARITY: Contains I response regulatory domain.
-i. CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A FRAMESHIFT IN POSITION 808.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-K12 / MG1655,
STRAIN-K12 / MG1655,
BIDLINE-742661). PubMed-9278503;
Biltiner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                       "Characterization of rcsB and rcsC from Escherichia coli 09:K30:H12 and examination of the role of the rcs regulatory system in expression of group I capsular polysaccharides.";
J. Bacteriol. 175:5384-5394(1993).
                                                                                                                                                                                                                                                                 Stout V., Gottesman S.; "RcsB and RcsC: a two-component regulator of capsule synthesis in Escherichia coli.";
                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                      RCSC_ECOLI STANDARD; PRT; 949 AA. PLASC_ECOLI STANDARD; P97645; P97170; P97225; Q47586; P01-3747; P99170; P97225; Q47586; P01-374-1990 (Rel. 13, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-FEB-2003 (Rel. 42, Last annotation update) Sensor protein rcsC (EC 2.7.3.-) (Capsular synthesis regulator component C).
                                                                                                                                                                                                                                                                                                                                                               MEDLINE-93374832; PubMed-8366025;
Jayaratne P., Keenleyside W.J., Maclachlan P.R., Dodgson C.,
Whitfield C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=K12;
MEDLINE=97251358; PubMed=9097040;
                                                                                                                                                                                                                                                  MEDLINE=90130299; PubMed=2404948;
                                                                                                                                                                                                                                                                                                         Bacteriol, 172:659-669(1990).
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=09:K30:H12;
                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                       Escherichia coli.
                                                                                                                                                                                              NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Probable).
                                                                                                                                       RCSC OR B2218
                                                                                                                                                                                                                                        STRAIN=K12;
           RESULT 5
RCSC_ECOLI
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940 REPONSE REGLIATORY.

479 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

875 PHOSPHORYLATION (BY SIMILARITY).

315 L -> V (IN STRAIN 09:K30:H12).

776 K -> E (IN STRAIN 09:K30:H12).

890 L -> Y (IN STRAIN 09:K30:H12).

938 L -> Y (IN STRAIN 09:K30:H12).

948 D -> E (IN STRAIN 09:K30:H12).

130 MT -> IN STRAIN 09:K30:H12).

131 MT -> IN STRAIN 09:K30:H12).

132 MT -> S (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane, Phosphorylation, Complete proteome. 19 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STIKKLREMEVKSMIVGVISLADNEEERRAFMEAGLNHCLAKPLIKDKI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00188; HATPASe_C; 1.
SMART; SM00188; HISRA; 1.
SMORT; SM00188; HISRA; 1.
SMART; SM00091; PASS: 1.
SMART; SM00041; PASS: 1.
PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50110; PAS, FALSE_NEG.
PROSITE; PS50110; RESPONSE_REGULATORY; 1.
Sensory transduction; Transferase; Manase; Bacterial capsule;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.3%; Score 171.5; DB 1; Length 949; 33.9%; Pred. No. 8.6e-07; Indels 32; Mismatches 37; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PERIPLASMIC (POTENTIAL).
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                                                                                                                                                                                                             EMBL, M28242; AAA24503.1; ALT_INIT.
EMBL, L11272; AAA24503.1; ALT_INIT.
EMBL, AE000311; AAC75278.1; ALT_INIT.
EMBL; D90850; BAA16001.1; ALT_ERAME.
EMBL; D90850; BAA16001.1; ALT_ERAME.
EMBL; D90851; BAA16009.1; ALT_ERAME.
EMBL; D90851; BAA16009.1; ALT_ERAME.
ENSE; P06143; 1UDR.
ECOGENDE, ED10822; CCC.
INTEPPO; DFR003594; ATPbind_ATPase.
INTEPPO; DFR003594; ATPbind_ATPase.
INTEPPO; IPR004369; Bact_Sens_pr_C.
INTEPPO; IPR004369; Bact_Sens_pr_C.
INTEPPO; IPR005467; His_Kinase.
INTEPPO; IPR000169; Response_reg.
Pfam; PF02518; HATPase_C; I.
Pfam; PF00372; HisKR; I.
Pfam; PF00372; HisKR; I.
PRINTS; PR00344; BCTRLEENOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
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FRZE_MYXXA
ID FRZE_MYXXA STANDARD;
AC P18769;
DT 01-NOV-1990 (Rel. 16, Created)
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э; Э

Gaps

ς. .. 14 KKLNVLIVDDDPLNLITHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPE 73

35.2%; Pred. No. 1.2e-05; ive 27; Mismatches 38; Indels

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Best Local Similarity 35.2
Matches 38; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                           PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
ALA/PRO-RICH (POSSIBLE HINGE REGION).
9912BD40991C69E5 CRC64;
                                                                                                                                   McCleary W.R., Zusman D.R.;
"FrzE of Myxococcus xanthus is homologous to both CheA and CheY of Salmonella typhimurium.";
                                                              Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESPONSE_REGULATORY; 1.
ion; Transferase; Kinase; Phosphorylation.
01-NOV-1990 (Rel. 16, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Gliding motility regulatory protein (EC 2.7.3.-).
                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 87:5898-5902(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESPONSE REGULATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HISTIDINE KINASE.
CHEW-LIKE.
                                                                           Cystobacterineae; Myxococcaceae; Myxococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; Q56310; 1B3Q.
InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR003594; Bact_sens_pr_C.
InterPro; IPR002545; Chew.
InterPro; IPR005467; His_kinase.
InterPro; IPR00570; Hpt.
InterPro; IPR001789; Response_reg.
Pfam; PF01584; Chew; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00344; BCTRISENSOR.
Prodom; PD000039; Response_reg; 1.
SMART; SM00260; CDEW; 1.
SMART; SM00387; HATPASE_C; 1.
SMART; SM00073; HPT; 1.
                                                                                                     [1]
SEQUENCE FROM N.A.
MEDLINE=90332690; PubMed=2165608;
                                                                                                                                                                                                                  MEDLINE-91072208; PubMed-2123853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01627; Hpt; 1.
Pfam; PF00072; response_reg; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83189 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS5081; CHBW; 1.
PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50894; HPT; 1.
PROSITE; PS50110; RESPONSE_RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; M35192; AAA25396.1; -.
                                                                                                                                                                                           [2]
PHOSPHORYLATION OF HIS-49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sensory transduction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A35966; A35966.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 1777 AA;
                                                   Myxococcus xanthus
                                                                                      NCBI_TaxID=34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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MOD_RES
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Score 156.5; DB 1; Length 777;

23.1%;

Query Match

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EMBO J. 13:5186-5194(1994).

-i. FUNCTION: INVOLVED IN OXIDATIVE STRESS. TRANSCRIPTION FACTOR THAT MAY FUNCTION IN A IWO-COMPONENT SIGNAL TRANSDUCTION PARHWAY THAT ACTS IN PARALLEL WITH THE PKC1 CASCADE TO REGULATE GROWTH AT THE CELL SURFACE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-94042854; PubMed=8226633;
Brown J.L., North S., Bussey H.;
"SKN7, a yeast multicopy suppressor of a mutation affecting cell wall
"SKN7, a yeast multicopy suppressor of a product with domains homologous to
beta-glucan assembly, encodes a product with domains homologous to
prokaryotic two-component regulators and to heat shock transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-S288C / AB972;
MEDLINE-94378003; PubMed-8091229;
MEDLINE-94378003; PubMed-8091229;
MEDLINE-94378003; PubMed-8091229;
Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J.,
Kucaba T., Hillier L., Jier M., Jöhnston L., Langskon Y.,
Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
Nhan M., Rifkin L., Riles L., St.Peter H., Trevaskis E., Vaughan K.,
Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-95045411; Pubmed-7957083;
Brown J.L., Bussey H., Stewart R.C.;
"Yeast Skn7p functions in a eukaryotic two-component regulatory
                                                                           74 RDGVSTTKKLREMEVKSMI - - VGVTSLADNEEERRAFMEAGLNHCLAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Krems B., Charizanis C., Entian K.-D.;
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                 SKN7_YEAST STANDARD; PRT, 622 AA.
P18889; P39747,
01.FEB-1995 (Rel. 31, Created)
01.FEB-1995 (Rel. 31, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative transcription factor SkN7 (PoS9) protein).
SKN7 OR POS9 OR BRY1 OR YHR206W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteriol. 175:6908-6915(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 265:2077-2082(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION, AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4932;
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SKN7_YEAST
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DOMAIN
TRANSMEM
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     69 KEMPERDGVSTIKKLREMEVKSMIVGVISLADNEEERRAFMEAGLNHCLAKPLIKDKI-- 126
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          MEDIINE-217:H7 / EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed-11206551;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Pavans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck B.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Appodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45; Indels 20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    R PRINTS; PRO0056; HGFDOMAIN;
R PATORN; PRO001788; HSF_DNA_bind; 1.
Prodom; PD0001788; HSF_DNA_bind; 1.
R RART; SM00415; HSF; 1.
SMART; SM00448; HSF DNAIN; 1.
R PROSITE; PS00434; HSF_DOMAIN; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Acrobic respiration control sensor protein arcB (EC 2.7.3.-).
Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.1%; Score 150; DB 1; Length 622; 28.1%; Pred. No. 3.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESPONSE REGULATORY.
PHOSPHORYLATION (PROBABLE).
D-N: IDMINISHED ACTIVITY.
D->E: AUGMENTED ACTIVITY.
4C732FD66E326742 CRC64;
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378 492 REG
427 427 PHG
427 427 D--
427 427 D--
622 AA; 69202 MW;
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ID ARCB_ECO57
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Best Local S
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MUTAGEN
MUTAGEN
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"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";

Nature 409:529-533(2001).

Re SEQUENE FROM N.A.

SEQUENE FROM N.A.

STRAIN-0157:H7 / RIMD 0509952;

RA MEDLINE-21156231; Pubbed-11258796;

RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., A. Hayashi T., Makino E., Nakayama K., Murata T., Tanaka M., Tobe T.,

A Hara S., Shiba T., Hattori M., Shinagawa H.; Fosenaga T.,

R. Ida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

R. A Kuhara S., Shiba T., Hattori M., Shinagawa H.; Escherichia coli

A Kuhara S., Shiba T., Hattori M., Shinagawa H.; Fasunaga T.,

R. Complete genome sequence of enterohemorrhagic Escherichia coli

O157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. SII-22(2001).

C 1-FUNCTION: Member of the two-component regulatory system arcB/arcA.

Sensor-regulator protein for anaerobic repression of the arc

modulon. Activates arcA via a four-step phosphorelay. ArcB can

modulon. Activates arcA via a four-step phosphorelay. ArcB can

c also dephosphorylate arcA vya v everse phosphorelay involving His-

C 1-SubcELLUAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Surpopen Bioinformatics Institute. There are no restrictions in its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       domain (By similarity).
-: SIMILARITY: Contains 1 histidine kinase domain.
-: SIMILARITY: Contains 1 her domain domain.
-: SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
-: SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
-: SIMILARITY: Contains 1 response regulatory domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 group from a His in the primary transmitter domain, to an Asp
the receiver domain and to a His in the secondary transmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- PIM: Activation requires a sequential transfer of a phosphate
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PROSITE; PS50113; PAC; 1.
PROSITE; PS50112; PAS; 1.
PROSITE; PS50110; RAS; 1.
PROSITE; PS50110; REPONSE_REGULATORY; 1.
Sensory transduction; Transferase; Kinase; Phosphorylation; Transmembrane; Inner membrane; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PERIPLASMIC (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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EMBL, AP002564; BAB37512.1; --
PIR, AP1140; AP1140.
PIR, D85885, D85985.
Interpro; IPR03594; ATPbind_ATPase.
Interpro; IPR003661; His_Kina.
Interpro; IPR005467; His_Kina.
Interpro; IPR00570; Hpt.
Interpro; IPR000700; PAS-assoc_C.
Interpro; IPR00014; PAS_domain.
Interpro; IPR001789; Response_reg.
Pfam; PF00518; Hiska; I.
Pfam; PF00518; Hiska; I.
Pfam; PF00572; response_reg; 1.
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ProDom; PD000039; Response_reg; 1.
SWART; SW00387; HATPRASe_c; 1.
SWART; SW00073; HPT; 1.
SWART; SW00091; PAS; 1.
SWART; SW00091; PAS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGREPMS; TIGRO0229; sensory_box; 1.
PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50894; HPT; 1.
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                                                                                                                                                                                       GVSTIKKLREMEVKSMIVGVTSLADNE-EERRAFMEAGLNHCLAKPLIKDKIIPLINQLM 134
                                                                                                                                               75
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES=E.coli; STRAIN=K12;
MEDLINE=90355832; PubMed=2201868;
Iuchi S., Matsuda Z., Fujiwara T., Lin E.C.C.;
"The arcB gene of Escherichia coli encodes a sensor-regulator protein
for anaerobic repression of the arc modulon.";
Mol. Microbiol. 4:715-727(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin O., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Ou D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and 0157."; Nucleic Acids Res. 30:4432-4441(2002)
                                                                                                                                                                                                   LNVLIVDDDPLNLITHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERD
                                                                                                                           3; Gaps
                                                 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SECULATES-E.COLI; STRAIN-KI2 / MG1655;
MEDLINE-97426617; PubMed-9278603;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V. Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                        Shigella flexneri.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                           01-AUG-1991 (Rel. 19, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Aerobic respiration control sensor protein arcB (EC 2.7.3.-).
ARCB OR B3210 OR SF3250.
                                                                                                      DB 1; Length 778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                           Indels
                                                                                 C8AE004B007F9D30 CRC64;
PAS.
PAC.
HISTIDINE KINASE.
RESPONSE REGULATORY.
HPT.
                                                                                                                ; Pred. No. 4.6e-05; 40; Mismatches 47;
                                                                                                                                                                                                                                                                                                         778 AA.
                                                                                                  Query Match 22.1%; Score 149.5; Best Local Similarity 25.6%; Pred. No. 4.6 Matches 31; Conservative 40; Mismatches
                                                                                 88010 MW;
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 2223
2278
2278
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771
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153 22 226 22 226 25 527 678 292 22 576 576 717 778 AA;
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Mau B., Shao Y.;
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P22763;
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MEDLINE-99047671; PubMed-9830034;
Georgellis D., Kwon O., De Wulf P., Lin E.C.C.;
"Signal decay through a reverse phosphorelay in the arc two-component signal transduction system.";
J. Biol. Chem. 273:32864-32869(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=E.col1;
MEDLINE-98437504; PubMed=9761838;
Rato M., Mizuno T., Hakoshima T.;
Crystallization of a complex between a novel C-terminal transmitter,
"Crystallization of a complex between a novel C-terminal transmitter,
"IPt domain, of the anaerobic sensor kinase ArcB and the chemotaxis response regulator CheY.";
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SPECIES-E.coli; STRAIN-K12 / MC4100;
MEDLINE-20309722; Pubmed=10851007;
Kwon O., Georgellis D., Lin E.C.C.;
Fhosphorelay as the sole physiological route of signal transmission
by the arc two-component system of Escherichia coli.";
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-:- SIMILARITY: Contains 1 HPT domain.
-:- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
-:- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
-:- SIMILARITY: Contains 1 response regulatory domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Probable).
--- PTM: Activation requires a sequential transfer of a phosphate group from a His in the primary transmitter domain, to an Asp the receiver domain and to a His in the secondary transmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES=E.col;/
MEDLINE=97207018; PubMed=9054511;
Rato M., Mizuno T., Shimizu T., Hakoshima T.;
Insights into multistep phosphorelay from the crystal structure the C-terminal HPt domain of ArcB.";
Cell 88:717-723(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 659-776 IN COMPLEX WITH
SPECIES=E.coli; STRAIN=M15;
MEDLINE=97431492; PubMed=9286997;
Georgellis D., Lynch A.S., Lin E.C.C.;
Georgellis D., Lynch A.S., Lin E.C.C.;
In vitro phosphorylation study of the arc two-component signal transduction system of Escherichia coli.";
J. Bacteriol. 179:5429-5435(1997).
[5]
CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.06 ANGSTROMS) OF 660-778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (1.57 ANGSTROMS) OF 659-776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acta Crystallogr. D 54:140-142(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIES=E.coli;
MEDLINE=20003135; Pubmed=10531481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       by the arc two-component system of
J. Bacteriol. 182:3858-3862(2000).
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RESULT 10
SLN1_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 LNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERD 75
                                                                                                                                                                                                                                                                                                         SMART; SM00073; HPT; 1.
SMART; SM00073; HPT; 1.
SMART; SM00073; HPT; 1.
SMART; SM00071; PAS; 1.
TIGREAMS; TIGR00229; sensory_box; 1.
TIGREAMS; TIGR00229; sensory_box; 1.
PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS50113; PAS; 1.
PROSITE; PS50113; PAS; 1.
PROSITE; PS50111; PAS; 1.
Sensory transduction; Transferase; Kinase; Phosphorylation; Transmembrane; Inner membrane; Transcription regulation; 3D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.1%; Score 149.5; DB 1; Length 778; 25.6%; Pred. No. 4.6e-05; ive 40; Mismatches 47; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION (AUTO-).
PHOSPHORYLATION (PROBABLE).
PHOSPHORYLATION (PROBABLE).
H->Q: LOSS OF ACTIVITY.
D->A: LOSS OF ACTIVITY.
H->Q: LOSS OF ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DD61EA6ECF95AD30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PERIPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HISTIDINE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISSING (IN REF
                                                          PDB: 1A0B: 18-MAR-98.
PDB: 1A0B: 17-JUN-98.
PDB: 1A0B: 17-JUN-98.
PDB: 1BC: 31-DEC-02.
PDB: 1ERO; 31-DEC-02.
ECGENCE: ECGENCE; arcel.
InterPro: IPR004359; ATPbind_ATPase.
InterPro: IPR004358; Bacc.sens.Pr.C.
InterPro: IPR001366; His. Kinas.
InterPro: IPR005467; His. Kinas.
InterPro: IPR001366; His. Kinas.
InterPro: IPR001366; His. Kinas.
InterPro: IPR001366; His. Kinas.
InterPro: IPR0001361; His. Kinas.
InterPro: IPR000104; PAS: acc.C.
InterPro: IPR00104; HAPRase.c.; I.
Pfam: PP00512; His.Ki. I.
Pfam: PP00969; PAS: 1.
Pfam: PP00969; PAS: 1.
ProDom: PP000134; BCTRLSENOR.
PP0DOM: PP000034; BCTRLSENOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
           EMBL; 018997; AAAJOULL.,
EMBL; AE000400; AA76242.1; -.
EMBL; AE015336; AAN44715.1; -.
PIR; D65112; RGECAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87982 MW;
 X53315; CAA37397.1; -. 018997; AAA58012.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 25.6
les 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         778 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome. DOMAIN 1
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DOMAIN
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SIM. PREST

OF 1728-1959 (Rel. 13, Cars Sequence update)

OF 1728-1959 (Rel. 14) Cars Sequence update)

OF 1728-1959 (Rel. 15) Cars Sequence update)

OF 1729-1959 (Rel. 15) Cars Sequence update)

OF 1729-19
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Page 10

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Matches
  SOURTH THE FEET TO DESCRIBE TO THE FEET THE PROPERTY OF THE PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 SSFDLILMDKEMPERDGVSTTKKL-REMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 DIEKIKKKLNVLIVDDDPLNLIIHEKIIKA---IGGIS--QTANNGEEA---VIIHRDGG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44; Indels 14; Gaps
                                                                                                                                                                                                                                                                                                                        CUTOPLASMIC (POTENTIAL).
HISTIDINE KINASE.
RESPONSE REGULATORY.
PHOSPHORYLATION (AUTO-) (PROBABLE).
PHOSPHORYLATION (PROBABLE).
N-LINKED (GLCNAC. ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND MUTAGENESIS.
MEDLINE-94239498; PubMed-8183345;
Maeda T., Wurgler-Murphy S.M., Saito H.;
Atoo-component system that regulates an osmosensing MAP kinase cascade in yeast.";
Nature 369:242-245(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H->Q: INACTIVE.
G->D: SLOW GROWTH, SLN1-1 MUTANT.
D->N: INACTIVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 145; DB 1; Length 1220; Pred. No. 0.00018;
                                                                                                                                                            PROSITE: PS50109; HIS_KIN; 1.
PROSITE; PS50110; RESPONSE_REGULATORY; 1.
Sensory transduction; Transferase; Kinase; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            134434 MW; 45FFE24A8165486B CRC64;
                                                                                                                                                                                                                                                                       POTENTIAL.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSK1_YEAST STANDARD; PRT; 712 AA. 007084; 007989; 01-00v-1997 (Rel. 35, Created) 01-Nov-1997 (Rel. 35, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Osomolarity two-component system protein SSK1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40; Mismatches
           Pfam: PF00512; HiskA: 1.
Pfam: PF0072; response_reg; 1.
PRINTS; PR00344; BCTRLSENSOR.
ProDom; PD000039; Response_reg; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [2]
SEQUENCE FROM N.A.
STRAIN=S288C / AB972;
MEDLINE=97313267; PubMed=9169871;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.4%;
29.0%;
                                                                                                  SMART; SM00387; HATPASE_C; 1
SMART; SM00388; HiSKA; 1.
SMART; SM00448; REC; 1.
PF02518; HATPase_c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1220 AA;
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Best Local Similarity
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                                                                                                                                                                                                                          Transmembrane.
DOMAIN
TRANSMEM 2
DOMAIN 4
TRANSMEM 333
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CARBOHYD
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MOD_RES
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Dohnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W., Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A., Benes V., Elana K.-D., Flocath M., Goffeau A., Hebling U., Hemmann K., Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P., Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D., Nortwich U., Obermale B., Piravandi E., Pohl T.M., Portetelle D., Purnelle B., Rechman S., Rieger M., Rinke M., Rose M., Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S., Uncertones B., Scholler P., Schwager C., Schwarz S., Noet M., Volckaart G., Voss H., Wambutt R., Wedler E., Medler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.; The nucleotide sequence of Saccharonyces cerevisiae chromosome XII."; The nucleotide sequence of Saccharonyces cerevisiae chromosome XII."; The nucleotide sequence of Saccharonyces cerevisiae chromosome XII."; Thurte 387:87-90(1997).

SINI/SSKI ACTIVATED BY CHANGES IN THE OSMOLARITY OF THE EXTRACELLULAR ENVIRONMENT. THIS SYSTEM CONTROLS THE SSK2/SSK22-SHOGI PATHWAY. THE UNBOSCHORYLATED STRANDELLIN BY SINI. MAPK CASCADE. IN LOW-OSMOLARITY MEDIA, IN INIBITED THERDUGH THE CHANGES IN LOW-OSMOLARITY MEDIA, IN INIBITED THEOUGH THE CHANGES IN THE CHANGE THE PBS2-HOGI MAPK CASCADE. IN LOW-OSMOLARITY MEDIA, IN INIBITED THEOUGH THE CHANGE CHANGE CHANGES IN THE CHANGE OF THE CHANGE C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         556 QLPVLSGIEAAKQIRDFEKQNGIGIQKSLNNSHSNLEKGTSKRFSQAPVIIVALTASNSQ 615
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EMBL; CAA97528.1; -.
PIR; S64828; S64828.
SGD; S0003996; SSK1.
GO; GO:0007234; P:Osmosensory signaling pathway via two-compo. .; IDA.
GO; GO:0042542; P:Issponse to hydrogen peroxide; IMP.
InterPro; IPR001789; Response_reg.
Pfam; PF00072; response_reg; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 EKIKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDK
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D->N: ACTIVATES.
P -> S (IN REF. 1).
F 33B2DBB4FCF2528A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBGNIT: SEEMS TO INTERACT WITH SSK2 AND SSK22.
-!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-!- SIMILARITY: Contains 1 response regulatory domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESPONSE REGULATORY
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01-FEB-1996 (Rel. 33, Last sequence update)
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SMART; SM00448; REC; 1.
PROSITE; PS50110; RESPONSE_REGULATORY; 1.
Sensory transduction; Phosphorylation.
DOMAIN 505 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 EEERRAFMEAGLNHCLAKPL 121
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712 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39;
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P48027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOD_RES
MUTAGEN
CONFLICT
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Best Local
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GACS_PSESY
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284
707
853
284 2
707 7
853 8
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SEQUENCE FROM N.A.
STRAIN=168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria;
MOD_RES
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SEQUENCE
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ID DCTR_B
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                                                                                                                                                                                                                                                                                                         PTM: Activation requires a sequential transfer of a phosphate group from a His in the primary transmitter domain, to an Asp in the receiver domain and to a His in the secondary transmitter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R HSSP; PO6143; IUDR.

InterPro; IPR003569; Bact_sens_pr_C.
InterPro; IPR003669; HAMP.

InterPro; IPR003671; His_Kinase.

R InterPro; IPR001799; Response_reg.

R Pfan; PF00512; HAMP; I.

R Pfan; PF00344; BAMP; I.

R SMART; SM00344; BAMP; I.

R SMART; SM00387; HATPase_c; I.

R SMART; SM00387; HATPase_c; I.

R SMART; SM00387; HATPase_c; I.

R SMART; SM00448; REC; I.

R R RANT; SM00448; REC; I.

R R RANT; SM00448; REC; I.

R R RANT; SM00448; HAMP; I.

R R RANT; SM00448; HAMP; I.

R R RANT; SM00448; HAMP; I.

R RANT; SM00448; HAMP; I.

R RANT; SM00448; HAMP; I.

R RANGITE; PS50894; HPT; I.

R RANGITE; PS50894; HPT; I.

R RANGITE; PS50804; HAMP; I.
                                                                                        Pseudomonas syringae (pv. syringae).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domain (By similarity).
-- SIMILARITY: Contains 1 HAMP domain.
-- SIMILARITY: Contains 1 histidine kinase domain.
-- SIMILARITY: Contains 1 HPT domain.
-- SIMILARITY: Contains 1 response regulatory domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HISTIDINE KINASE.
RESPONSE REGULATORY.
HPT.
28-FEB-2003 (Rel. 41, Last annotation update)
Sensor protein gacs (EC 2.7.3.-).
GACS OR LEMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
POTENTIAL.
HAMP.
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                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-92234961; PubMed-1314807;
Hrabak E.M., Willis D.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Inner membrane.
                                                                                                                                                      Pseudomonadaceae; Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M80477; AAA25877.1; -. HSSP; P06143; 1UDR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane;
TRANSMEM 9
TRANSMEM 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Probable).
                                                                                                                                                                                   NCBI_TaxID=321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ON BEAN.
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THE HAM WAND BRANK ```

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69 KEMPERDGVSTTKKLREMEVKS-----MIVGVTSLADNEEERRAFMEAGLNHCLAKPLTK 123
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Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borliss R., Boursier L., Brans A., Braun M., Brignells C., Bron S.,
Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connecton I.F., Cummings N.J., Daniel R.A.,
RA Chian K.D. Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Fitz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Grandi G.,
RA Fitz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Grandi G.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Iraya M., Jones L.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Iraya M., Jones L.,
RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
R., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Median N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Setor M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie F.,
RA Sator T., Scanlan E., Schleich S., Schroeter R., Yasamott A.,
RA Sarokin A., Tanaka H., Takamashi H., Takamaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Yasamott R.,
Winners P., Wipat A., Yamamoto H., Yamane K., Yasumoto R., Yata K.,
RA Viari A., Wambutt R., Wadher H., Weitzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto R., Yasumoto H., Yakanan H., Rayanan H., Rayanan H., Rayanan H., Rayanane R., Yoshikawa H., Nashikawa H., Nashikawa H., Rayanane R., Yoshikawa H., Yasumoto H., Yasumoto R., Yasumoto R., Yasumoto R., Yoshikawa H., Yasumoto R., Y
                                                                                                                                                                                                                                                                                                                                                                                                                                 18 VLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGG------SSFDLILMD 68
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
PHOSPHORYLATION (BY SIMILARITY).
FROSPHORYLATION (BY SIMILARITY).
5 SB9F4663DAF3492C CRC64;
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rasahara Y., Nakai S., Lee S., Sadaie Y., Ogasawara N.;
"A 148 kbp sequence of the region between 35 and 47 degree of
Bacillus subtilis genome.";
                                                                                                                                                                                                                                          20.9%; Score 142; DB 1; Length 907; 27.6%; Pred. No. 0.00023;
                                                                                                                                                                                                                                                                                                                                     33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus subtilis genome.";
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DCTR_BACSU STANDARD; PRT; 226 AA.
P96602; P94503;
16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
28-FRB-2003 (Rel. 41, Last annotation update)
Probable C4-dicarboxylate response regulator dctR.
                                                                                                                                                                                                                                                                                                                                          33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-98044033; PubMed-9384377;
                                                                                                                                                   99195 MW;
                                                                                                                                                                                                                                          Query Match
Best Local Similarity 27.68
Matches 35; Conservative
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A COC OS OS A COC OS OS A COC OS OS A COC OS A C
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                                                                                                                                                                                                                                                                                                                                                                                                     Regularization of the Iransport system for the uncarboxylte actus. In Regularization of the Uncolology 146:263-274(2000).

Microbiology 146:263-274(2000).

INCOTOLIAN MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM DCTS/DCTR.

ESSENTIAL FOR EXPRESSION OF DCTP.

ISSENTIAL FOR EXPRESSION OF DCTS (FROBABLE).

ISSENTIAL FOR CATAINED BY DCTS (FROBABLE).

I SIMILARITY: Contains 1 response regulatory domain.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 KKKLNVLIVDDDPLNLIIHEKIIKAIGGIS--QTANNGEEAVIIHRDGGSSFDLILMDKE 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 MPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKI 126
"The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.";
                                                                                                                                                                                                                                                                                                                                 MEDLINE=20170658; PubMed=10708364; Asai K., Baik S., Ogasawara N.; Asai K., Baik S.-H., Kasahara Y., Moriya S., Ogasawara N.; Regulation of the transport system for C4-dicarboxylic acids in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
2;
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SMART; SM0446, REC; I.

PROSITE; PS50110; RESPONSE_REGULATORY; I.

PROSITE; PS50110; Transcription regulation; DNA-binding;
Activator; Phosphorylation; Complete proteone.

7 123 RESPONSE REGULATORY.

MOD_RES 58 BHOSPHORYLATION (BY SIMILARITY).

DNA_BIND 76 206 HFT-H MOTIF (POTEWITAL).

CONFLICT 24 F -> I (IN REF. 3).

SEQUENCE 226 AA; 25539 MW; 018115B14E9ER47D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.7%; Score 140.5; DB 1; Length 226; 25.9%; Pred. No. 6.7e-05; ive 39; Mismatches 42; Indels 5
                                                                                                                                                                      Morel-Deville F., Ehrlich S.D., Morel P.; "Identification by PCR of genes encoding multiple response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, 299106; CAB12253.1; --
EMBL, 102580; AAB47751.1; --
FIR B69771; B69771.
FISP, Q56312; 1TMY.
Subtilist; B612074; dctR.
Interpro; IPR001789; Response_reg, IPR0178; PF00072; response_reg, IPRSF; PIRSF006171; RR_citrat_malat; 1.
                                                                                                                                            MEDLINE-97311990; PubMed-9168601;
                                                                                                                                                                                                                                              Microbiology 143:1513-1520(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB001488; BAA19283.1; -.
                                                                                                  SEQUENCE OF 14-101 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                   Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                             FUNCTION, AND GENE NAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001
16-OCT-2001
28-FEB-2003
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Q9K998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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DCTR_BACHD
ID DCTR_BA
AC 09K998;
DT 16-OCT-
DT 18-OCT-
DT 28-FEB-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Horixoshi K.;
"Complete genome sequence of the alkaliphilic bacterium Bacillus "Complete genome sequence comparison with Bacillus subtilis.";
halodurans and genomic sequence comparison with Bacillus subtilis.";
Nucleic Acids Res. 28:4317.4331(2000).
-: FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM DCTS/DCTR...
ESSEMITAL FOR EXPRESSION OF DCTP (BY SIMILARITY).
-: SUBCELLULAR LOCATION: Cytoplasmic (Potential).
-: PTM: PHOSPHORYLATED BY DCTS (BY similarity).
-: SIMILARITY: Contains I response regulatory domain.
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                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N., Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sensory transduction; Transcription regulation; DNA-binding; Sensory transduction; Transcription regulation; DNA-binding; Activator; Phosphorylation; Complete proteome.

DOMAIN 8 124 RESPONSE REGULATORY.

MOD RES 59 59 FINCSPHORYLATION (BY SIMILARITY).

DIAL_BIND 183 209 H-T-H MOTIF (POTENTIAL).

SEQUENCE 230 AA; 26376 MM; 06FD65F46FC57D40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
                                                                                                        Bacillales; Bacillaceae; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 20.7%; Score 140.5; DB 1; Best Local Similarity 29.4%; Pred. No. 6.9e-05; Matches 35; Conservative 32; Mismatches 47;
Probable C4-dicarboxylate response regulator dctR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHEY_BACSU STANDARD; PRT; 119 AA. p24072; P3783; COL-MAR-1992 (Rel. 21, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 28-PEB-2003 (Rel. 41, Last annotation update) CHEY OR CHEB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AP001516; BAB06470.1; -. PTR; G83993; G83993.
HSSP; PI0957; IRNL.
InterPro; IPR001789; Response_reg.
Pfam; PF00072; response_reg; 1.
PTGSF; PIRSFOORTI, RR_catrat_malat; 1.
ProDom; PD000039; Response_reg; 1.
SMART; SN00448; REC; 1.
                                                                                                        Bacteria; Firmicutes;
NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
STRAIN=168 / OI1085;
                                                                     Bacillus halodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1423;
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SEQUENCE OF 1-12.
SERAIN-168 / JH642;
MEDLINE=96445629; Pubmed=8755892;
Graumann P., Schroeder K., Schmid R., Marahiel M.A.;
Groud shock stress-induced proteins in Bacillus subtilis.";
J. Bacteriol. 178:4611-4619(1996).
I. TS HOWOLOGOUS TO THE CHEY PROTEIN OF OTHER BACTERIA, IT IS
THOUGHT TO FUNCTION IN A DIFFERENT MANNER.
I. SUBCELLULAR LOCATION: Cytoplasmic.
I. SIMILARITY: Contains 1 response regulatory domain.
This SHISS-PROT entry is copyright. It is produced through a Collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation
                                                                                                                                                                                             Minchiller F., Ogaawara N. G., Bessleres P., Bolotin A., Alloni G., Azevedo V., Bertero M.G., Bessleres P., Bolotin A., Borchert S., Barsedo V., Bertero M.G., Bessleres P., Bolotin A., Borchert S., Borriss R., Boursier L., Brans A., Brain M., Brighell S.C., Bron S., Bronillet S., Bruschi C. V., Caldwell B., Capuano V., Carter N. M., Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A., Britan K.D., Errington J., Fabret C., Ferrari E., Foulger D., Annings N.J., Daniel R.A., Britan K.D., Errington J., Fabret C., Ferrari E., Foulger D., Annings N.J., Grandi G., Guiseppi G., Guy B.J., Haga K., Galighily B.J., Grandi G., Guiseppi G., Guy B.J., Haga K., Halooh J., Harwood C.R., Henaut A., Hibert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., As Anningstein G., Karamata D., Kasahara Y., Kaerrer Blandohard M., Klein C., Robyashi Y., Koetter P., Koningstein G., Kawano M., Klein C., Mediud R., Lardinois S., Lauber J., Lazarevic V., Railada R.P., Mizun M., Moestl D., Nakai S., Noback M., Brescan E., Pull H., Masuda S., Mauel C., Medigue C., Medina N., Pohlado R.P., Mizun M., Moestl D., Nakai S., Noback M., Prescon E., Puller B., Roche B., Rose M., Sadale Y., Prescan E., Pulle C., Roche B., Roche B., Rock B., Reynolds S., Schrocher R., Scoffone F., Sato T., Scanlan E., Schleich S., Schrocher R., Schrömer K., Scoffone F., Seriech S., Schrocher R., Scokin A., Tacconi E., Takadi T., Tarahashi H., Takamaru K., Takahashi H., Takamaru K., Takakeuti M., Tamakoshi A., Tanaka T., Terpstra P., Malbut R., Wedler E., Wedler H., Weitzeneger T., Wilters P., Wilata A., Sarotor P., Salmoto K., Yasumoto M., Yoshida K., Yamamoto G. the Gram-positive bacterium Bacillus W. Welling R., Yoshida K., Yasumoto G. the Gram-positive bacterium Bacillus R., Wellin B.
MEDLINE-91286247; PubMed-1905718; Baschoff D.S., Ordal G.W. "Sequence and characterization of Bacillus subtilis CheB, a homolog of Escherichia coli CheY, and its role in a different mechanism of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=168 / OI1085;
MEDLINE=93078625; PubMed=1447979;
Bischoff D.S., Ordal G.W.,
Identification and characterization of FliY, a novel component of the Bacillus subtilis flagellar switch complex.";
MOI. Microbiol. 6:2715-2723(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=168 / OI1085;
MEDLINE-92289757; PubMed-1597417;
Bischoff D.S., Weinreich M.D., Ordal G.W.;
"Nucleotide sequences of Bacillus subtilis flagellar biosynthetic
genes flip and fliQ and identification of a novel flagellar gene,
                                                                                chemotaxis.";
J. Biol. Chem. 266:12301-12305(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriol. 174:4017-4025(1992).
                                                                                                                                                                                     MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 95-119 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 390:249-256(1997).
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                                                                                                                                             SEQUENCE FROM N.A.
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 VLIVDDDP-LNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 VSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLINQLMD 135
                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00448; REC; 1.
PROSITE; PS50110; RESPONSE_REGULATORY; 1.
Chemotaxis; Sensory transduction; Phosphorylation; Complete proteome.
INIT_MET 0 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0 0 RESPONSE REGULATORY.
1 118 PHOSPHORYLATION (BY SIMILARITY).
119 AA; 13178 MW; F3BCAOFO2CAB7531 CRC64.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.8%; Score 134; DB 1; Length 119; 26.9%; Pred. No. 0.00012; Live 36; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: August 13, 2003, 19:11:30 Job time : 12 secs
                                                                                                                                                           EMBL, M59781; AAA22311.1; -.
EMBL; 299112; CAB13506.1; -.
EMBL; M66738; AAA22450.1; -.
EMBL; M67005; AAA22451.1; -.
PIR; A40874; A40874.
Subtilist; B610258; chey.
Interpro; IPR001789; Response_reg.
                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00072; response_reg; 1.
ProDom; PD000039; Response_reg; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

August 13, 2003, 19:09:22 ; Search time 37 Seconds (without alignments) 948.518 Million cell updates/sec

Run on:

US-09-646-679-15 678 1 MATKSMGDIEKIKKKINVLI......LAKPLTKDKIIPLINQLMDA 136 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

830525 seqs, 258052604 residues Searched:

830525 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

sp\_virus:\*
sp\_vertebrate:\*
sp\_unclassified:\*
sp\_rvirus:\*
sp\_bacteriap:\*
sp\_archeap:\* SPTREMBL\_23:\*
1: sp\_archea:\*
2: sp\_bacteria:\*
3: sp\_fungi:\*
4: sp\_human:\*
5: sp\_invertebrate:\* sp\_mhc:\*
sp\_organelle:\* sp\_rodent:\* sp\_mammal:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

|                               | ď                  | Ø                  |             |                   | Ø                  | н            | ଷ            |                    | ø                  | ψ            |             | ຜ                  | Ø            |             | w            | н            |
|-------------------------------|--------------------|--------------------|-------------|-------------------|--------------------|--------------|--------------|--------------------|--------------------|--------------|-------------|--------------------|--------------|-------------|--------------|--------------|
| ption                         | 082445 brassica na | Q9m8y4 arabidopsis | dictyosteli | Q8ez63 leptospira | Q8cvu5 escherichia | 0 caulobacte | 9 escherichi | Q9rlc7 pseudomonas | Q8xe39 escherichia | 4 yersinia p | vibrio fisc | 08pg37 xanthomonas | 8 xanthomona | proteus mir | 3 xanthomona | 2 caulobacte |
| Description                   | 08244              | , y 8 m 8 y        | 015763      | Q8ez6.            | QBcvu              | Q9a3p(       | Q8ffp        | Q9rlc7             | Q8xe3              | Q8zgr        | Q9any0      | .68bd3.            | 08bju        | 085663      | 88480        | 09a31        |
| ID                            | 082445             | Q9M8Y4             | 015763      | Q8E263            | Q8CVU5             | Q9A3P0       | Q8FFP9       | Q9RLC7             | O8XE39             | 082GR4       | Q9ANY0      | Q8PQ37             | QBPJN8       | 085663      | Q8P883       | 09A3L2       |
| DB                            | 10                 | 10                 | S           | 16                | 16                 | 16           | 16           | (7                 | 16                 | 16           | 7           | 16                 | 16           | Ŋ           | 16           | 16           |
| %<br>Query<br>Match Length DB | 136                | 142                | 1969        | 820               | 1197               | 394          | 949          | 417                | 933                | 957          | 927         | 769                | 1364         | 507         | 1364         | 642          |
| %<br>Query<br>Match           | 100.0              | 79.4               | 26.7        | 26.5              | 26.3               | 25.7         | 25.6         | 25.5               | 25.3               | 25.3         | 25.2        | 25.1               | 24.7         | 24.6        | 24.1         | 24.0         |
| Score                         | 678                | 538                | 181         | 179.5             | 178.5              | 174          | 173.5        | 173                | 171.5              | 171.5        | 171         | 170                | 167.5        | 166.5       | 163.5        | 162.5        |
| Result<br>No.                 |                    | 73                 | m           | 4                 | S                  | φ            | 7            | æ                  | מי                 | 10           | 11          | 12                 | 13           | 14          | 15           | 16           |
|                               |                    |                    |             |                   |                    |              |              |                    |                    |              |             |                    |              |             |              |              |

| Q9p896 emericella | Q8zb69 yersinia pe | Q8pd62 xanthomonas | Q9gtuO dictyosteli | Q95ph5 dictyosteli | Q8d5i6 vibrio vuln | Q8d9h9 vibrio vuln |      | 028381 archaeoglob |         | Q8yyw3 anabaena sp | Q8n1v2 neurospora | Q9ac40 caulobacter | Ωч       |      |      | Q8qkv7 ectocarpus | 028887 archaeoglob | Q9ks16 vibrio chol | Q9c1q7 aspergillus | Q9aew3 pseudomonas | Q9a472 caulobacter | Q8kws5 marinomonas | Q8kgv0 vibrio chol | Q48299 halobacteri |         |            | Q8rmf4 acinetobact | Q8pmz3 xanthomonas |
|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|------|--------------------|---------|--------------------|-------------------|--------------------|----------|------|------|-------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|---------|------------|--------------------|--------------------|
| м                 | 16                 | 16                 | ហ                  | Ŋ                  | 16                 | 16                 | 16   | Н                  | 16      | 16                 | m                 | 16                 | ~        | 17   | 16   | 12                | 17                 | Г                  | m                  | Ŋ                  | 16                 | 7                  | 7                  | 17                 | 9⊺      | <b>J</b> 6 | 7                  | 16                 |
| .5 24.0           | 24.0               | 23.9               | 23.8               | 23.8               | 23.7               | 23.7               | 23.5 | 23.5               | 59 23.5 | 23.5               | 23.4              | 23.2               | 6.5 23.1 | 23.0 | 22.9 | 22.9              | 4.5 22.8           | 4.5 22.8           | 22.7               | 2.7                | 3.5 22.6           | 3.5 22.6           | 53 22.6            | .5 22.5            | .5 22.5 | .5 22.5    | 22.                | .5 22.5            |
| 17 16             |                    |                    |                    |                    |                    |                    |      | 25                 | 56      | 27                 | 15                |                    | 15       |      |      |                   | 34 15              | 35 15              | 98                 | 37                 | 38 15              | 39 15              | 40                 | П                  | 42 15   | П          | 44 15              | 45 15              |

### ALIGNMENTS

| % Created) 08, Created) 29, Last annoein. 29, Last annoein. e; Streptophyt phyta; eudicot s; Brassicacea requience r |           |                                                     |                     |                         |
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| 998 (TrEMBLrel. 08, Created) 998 (TrEMBLrel. 08, Last sequence update) 102 (TrEMBLrel. 22, Last annotation update) 103 (TrEMBLrel. 22, Last annotation update) 104 (TrEMBLrel. 22, Last annotation update) 105 (TremBlator protein. 105 (TremBlator protein. 106 (TremBlator protein. 107 (TremBlator protein. 108 (TremBlator protein. 109 (TremBlator protein. 100 (TremBlator protein. 109 (TremBlator protein. 109 (TremBlator protein. 100 (TremBlator pr |           | PRELIMINARY; PRT;                                   | 136 AA.             |                         |
| 102 (TERBELFel. 22, Last annotation update) 11 regulator protein. 12 regulator protein. 13 Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; 12 Viridiplantae; Streptophyta; Embryophyta; Care eudicots; Rosidae; 11; Brassicales; Brassicaceae; Brassica. 12 Brassicales; Brassicaceae; Brassica. 13 Brassicales; Brassicaceae; Brassica. 14 Brassicales; Brassicaceae; Brassica napus is ared during pod development." 15 Brassicales; Brassicaceae; Brassica napus is ared during pod development." 16 (APR.1998) to the EMBL/GenBank/DDBJ databases. 17 AAC6225.1; Care EMBL/GenBank/DDBJ databases. 18 (APR.1998) Response_reg. 18 (APR.1998) Response_reg. 19 PR0001789; Response_reg. 100003; Response_reg. 100003; Response_reg. 11 PR001789; Response_reg. 13 AAC6225.1; Cared. 10 Cared. | 99        | (TremBLrel. 08, (TremBLrel. 08,                     | d)<br>equence upó   | late)                   |
| regulator protein.  nagus (Rape).  y Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  y Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  II; Brassicales; Brassicaceae; Brassica.  II; Brassicales; Brassicaceae; Brassica.  C.A., Paul W., Jenkins E.S., Taylor V.M., Roberta J.A.;  EROM N.A.  C.A., Paul W., Jenkins E.S., Taylor V.M., Roberta J.A.;  ated during pod development.",  A (APR.1998) to the EMBL/GenBank/DDBJ databases.  B (APR.1998) to the EMBL/GenBank/DDBJ (APR.1998)  A (APR.1998) to the EMBL/GenBank (APR.1988)  A (APR.1998) to the EMBL/GenBank (APR.1998)  A (APR.1998) to the EMBL/Ge | õ         |                                                     | nnotation           | ıpdate)                 |
| wiridiplantae; Streptophyta; Embryophyta; Tracheophyta; D=3708; ENDM N.A. C.A., Paul W., Jenkins E.S., Taylor V.M., Roberta J.A.; EROM N.A. C.A., Paul W., Jenkins E.S., Taylor V.M., Roberta J.A.; EROM N.A. C.A., Paul W., Jenkins E.S., Taylor V.M., Roberta J.A.; A.C.A.; Paul W., Jenkins E.S., Taylor V.M., Roberta J.A.; A.C.A.; Paul W., Jenkins E.S., Taylor V.M., Roberta J.A.; A.C.A.; Paul W., Jenkins E.S., Taylor V.M., Roberta J.A.; A.C.A.; Paul W., Jenkins E.S., Taylor V.M., Roberta J.A.; A.C.A.; Paul W., Jenkins E.S., Taylor V.M., Roberta J.A.; A.C.A.S. T. Taylor V.M., DA998768FABBGFF5 CRC64; A.J. Taylon; Sensory transduction. Ylation; Sensory transduction. Ylation; Sensory transduction. Ylation; Sensory transduction. A.J. Taylor V. Taylor V.A., Ta |           | legulator protein.<br>Japus (Rape),                 |                     | ,                       |
| Ditta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;  II; Brassicales; Brassicaceae; Brassica.  Di=3708;  FROM N.A.  C.A., Paul W., Jenkins E.S., Taylor V.M., Roberts J.A.;  C.A., Paul W., Jenkins E.S., Taylor V.M., Roberts J.A.;  C.A., Paul W., Jenkins E.S., Taylor V.M., Roberts J.A.;  C.A., Paul W., Jenkins E.S., Taylor V.M., Roberts J.A.;  C.A., Paul W., Jenkins E.S., Taylor V.M., Roberts J.A.;  C.A., Paul W., Jenkins E.S., Taylor V.M., Roberts J.A.;  C.A., Paul W., Jenkins E.S., Taylor V.M., Roberts J.A.;  GAPR-1998 to the EMBL/GenBank/DDBJ databases.  (APR-1998) to the EMBL/GenBank DBJ databases.  (APR-1998) to the EMBL/GenBank DBJ databases TAMBALLININININININININININININININININININI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | ď         | Viridiplantae; Streptopl                            | hyta; Embry         | ophyta; Tracheophyta;   |
| II; Brassicales; Brassicaceae; Brassica.  III; Brassicales; Brassicaceae; Brassica.  EROM N., Jonkins E.S., Taylor V.M., Roberts J.A.;  C.A., Paul W., Jenkins E.S., Taylor V.M., Roberts J.A.;  encoding a response regulator protein from Brassica napus is atted during pod development.";  d (APR-1998) to the EMBL/GenBank/DDBJ databases.  51PR001789; Response_reg.  51PR001789; Response_reg.  600072; response_reg.  61DR00139; Response_reg.  71DR00139; Response_reg.  72DR00033; Response_reg.  73DR00033; Response_ | ď         | lyta; Magnoliophyta; eudio                          | cotyledons;         | core eudicots; Rosidae; |
| FROM NA.  C.A., Paul W., Jenkins E.S., Taylor V.M., Roberts J.A.;  E.ROM NA.  C.A., Paul W., Jenkins E.S., Taylor V.M., Roberts J.A.;  Encoding a response regulator protein from Brassica napus is at (APR-1998) to the EMBL/GenBank/DDBJ databases.  J. PAG62225.1;  J. PAG62225.1;  J. PRO101789; Response_reg; 1.  MO042; Response_reg; 1.  MO048; REC; 1.  PRECIDING RESPONSE_REGULATORY; 1.  PRECIDIO, RESPONSE_REGULATORY; 1.  PRECIDIO RESPONSE_REGULATORY 1.  PRECIDE REGULATORY 1.                                     | S         | II; Brassicales; Brassicad                          | ceae; Brass         | 310a.                   |
| FROM N.A.  C.A., Paul W., Jenkins E.S., Taylor V.M., Roberts J.A.; ancoding a response regulator protein from Brassica napus is at (APR-1998) to the EMBL/GenBank/DDBJ databases.  3 (APR-1998) to the EMBL/GenBank/DDBJ databases.  5 IPR001789; Response_reg; 1.  500727; AAC62225.1;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | į.        | ,00,10                                              |                     |                         |
| C.A., Paul W., Jonkins E.S., Taylor V.M., Koderts J.A.;  ancoding a response regulator protein from Brassica napus is ated during pod development.";  ated during pod development.";  ated during pod development.";  ated during pod development.";  by 1057027; AAC62225.1;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | E         | ROM N.A.                                            |                     |                         |
| ancoding a response regulator protein from brassica napus is ated during pod development."  3 (APR-1998) to the EMBL/GenBank/DDBJ databases.  35 (APR-1998) to the EMBL/GenBank/DDBJ databases.  4 (APR-1998) to the EMBL/GenBank/DDBJ databases.  50 (ADS-10.1) to the EMBL/GenBank/DDBJ databases.  50 (ADS-10.2) to the EMBL/GenBank/DDBJ databases.  50 (ADS-10.2) to the EMBL/GenBank-TORY 1.  50 (ADS-10.2) to the EMBL/GenBank-TORY 1.  50 (ADS-10.2) to the EMBL/GenBank-TORY 1.  51 (ADS-10.2) to the EMBL/GenBank-TORY 1.  52 (ADS-10.2) to the EMBL/GenBank-TORY 1.  53 (ADS-10.2) to the EMBL/GenBank-TORY 1.  54 (ADS-10.2) to the EMBL/GenBank-TORY 1.  55 (ADS-10.2) to the EMBL/GenBank-TORY 1.  56 (ADS-10.2) to the EMBL/GenBank-TORY 1.  57 (ADS-10.2) to the EMBL/GenBank-TORY 1.  58 (ADS-10.2) to the EMBL/GENBANK-TORY 1.  59 (ADS-10.2) to the EMBL/GENBANK-TORY 1.  50 (ADS-10.2) to the EMBL/GENBANK-TORY 1.  51 (ADS-10.2) to the EMBL/GENBANK-TORY 1.  52 (ADS-10.2) to the EMBL/GENBANK-TORY 1.  53 (ADS-10.2) to the EMBL/GENBANK-TORY 1.  54 (ADS-10.2) to the EMBL/GENBANK-TORY 1.  55 (ADS-10.2) to the EMBL/GENBANK-TORY 1.  56 (ADS-10.2) to the EMBL/GENBANK-TORY 1.  57 (ADS-10.2) to the EMBL/GENBANK-TORY 1.  58 (ADS-10.2) to the EMBL/GENBANK-TORY 1.  58 (ADS-10.2) to the EMBL/GENBANK-TORY 1.  58 (ADS-10.2) to the EMBL/GENBANK-TORY 1.  59 (ADS-10.2) to the EMBL/GENBANK-TORY 1.  50 (ADS-10.2) to the EMBL/GENBANK-TORY 1.  51 (ADS-10.2) to the EMBL/GENBANK-TORY 1.  51 (ADS-10.2) to the EMBL/GENBANK-TORY 1.  51 (ADS-10.2) to the EMBL/GENBANK-TORY 1.                           | 3         | .A., Paul W., Jenkins E.                            | S., Taylor          | Koberta J.A.;           |
| Targed during you development;  (a) (APR-1998) to the EMBL/GenBank/DDBJ databases.  (b) (2027; AAC62225.1;  (c) (1) (1) (1) (1) (1) (1) (1) (1) (1) (1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ōi<br>⊲t: | scoding a response regular                          | tor proteir         | sica napus              |
| A                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | TT T      | ted during pod development                          | C.";                | T databases             |
| IPR001789; Response_reg.   O0072; Response_reg.   D00703; Response_reg.   O0072; Response_reg.   O0072; Response_reg.   O0072; Response_reg.   O0072; Response_reg.   O0072; Response_reg.   O0072; Response_reg.   O00748; REC.   O00748; REC.   O00748; REC.   O007448; REC.   O007448; REC.   O007448; REC.   O007448; REC.   O007448; REC.   O007448; REC.   O00744; REG.   O00744; REG   | A FO      | 57027: AAC62225.1:                                  | ,                   |                         |
| 00072; response_reg; 1.  #00448; REC; 1.  #0048; REC; 1.  #00.08; Pred. No. 4.7e-52;  #00.08; Pred. No. 4.7 | ro'.      | IPR001789, Response reg.                            |                     |                         |
| PD000039; Response_reg; 1.  M00448; REC; 1.  PS550110; RESPONSE_REGULATORY; 1.  PS550110; Sensory transduction.  136 AA, 15055 MW; DA99B768FAB3CFF5 CRC64;  100.0%; Score 678; DB 10; Length 136;  Similarity 100.0%; Pred. No. 4.7e-52;  6; Conservative 0; Mismatches 0; Indels 0; Gaps  MATKSMCDIEKTKKLNYLIVDDDPLNLIHEKTIKAIGGISQTANNGEBAVIIHEDGGS 60  MATKSMCDIEKTKKLNYLIVDDDPLNLIHEKTIKAIGGISQTANNGEBAVIIHEDGGS 60  MATKSMCDIEKTKKLNYLIVDDDPLNLIHEKTIKAIGGISQTANNGEBAVIIHEDGGS 60  SPDLILMDKEMPERDGVSTTKKLREMEVKSMIVGYTSLADNEEBERRAFMEAGLINHCLAKP 12                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | PF0       |                                                     |                     |                         |
| M00448; REC: 1. PS50110; RESPONSE_REGULATORY; 1. PS50110; RESPONSE_REGULATORY; 1. 136 AA; 15055 MW; DA99B768FAB3CFF5 CRC64; 100.0%; Score 678; DB 10; Length 136; Similarity 100.0%; Pred. No. 4.7e-52; 6; Conservative 0; Mismatches 0; Indels 0; Gaps MATKSMGDIEXIKKLNVLJVDDDPLNLIIHEKIIKAIGGISQTANNGEBAVIIHRDGGS 60                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | <u></u>   |                                                     |                     |                         |
| PS5011D; RESPONSE_REGULATORY;  136 AA; 15055 MW; DA998768FAB3CFF5 CRC64;  136 AA; 15055 MW; DA998768FAB3CFF5 CRC64;  100.0%; Score 678; DB 10; Length 136;  Similarity 100.0%; Pred. No. 4.7e-52; Indels 0; Gaps  MATKSMGDIEKIKKRNVLIVDDDPLNLIHEKIIKAIGGISQTANNGEBAVIHRDGGS 60  MATKSMGDIEKIKKLNVLIVDDDPLNLIHEKIIKAIGGISQTANNGEBAVIHRDGGS 60  SFDLILMDKEMPERDGYSTFKIREMEVYSMIVGYTSLADNEEBERAFMEGLINHCLAKP 12  SFDLILMDKEMPERDGYSTFKKIREMEVKSMIVGYTSLADNEEBERAFMEGLINHCLAKP 12  SFDLILMDKEMPERDGYSTFKKIREMEVKSMIVGYTSLADNEEBERAFMEGALINHCLAKP 12  SFDLILMDKEMPERDGYSTFKKIREMEVKSMIVGYTSLADNEEBERAFMEAGLINHCLAKP 12                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | SM        | 00448; REC; 1.                                      |                     |                         |
| ylation; Sensory transduction.  136 AA; 15055 MW: DA99B768FAB3CFF5 CRC64;  100.0%; Score 678; DB 10; Length 136;  Similarity 100.0%; Pred. No. 4.7e-52; Indels 0; Gaps 6; Conservative 0; Mismatches 0; Indels 0; Gaps  MATKSMCDIEKIKKLNYLIVDDPLNILIHEKIIKAIGGISQTANNGEBAVIIHEDGGS 60  HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | <br>ш     | SSO110; RESPONSE_REGULAT                            | ORY; 1.             |                         |
| Similarity 100.0%; Score 678; DB 10; Length 136; Gaps 6; Conservative 0; Mismatches 0; Indels 0; Gaps Matksmodlektkknvljvdddplullihekiikaiggisqranngebaviihrdggs 60   Hill                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | Ory       | lation; Sensory transduct.<br>136 AA: 15055 MW: DA9 | 10n.<br>98768FAB3CI | FFS CRC64;              |
| Similarity 100.0%; Pred. No. 4.7e-52; 6; Conservative 0; Mismatches 0; Indels 0; Gaps MATKSMGDIEXIKKKLNVLJVDDDPLNLIIHEKIIKAIGGISQTANNGEBAVIIHRDGGS 60 MATKSMGDIEXIKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEBAVIIHRDGGS 60 SPDLILMDKEMPERDGVSTTKKLRDEWEVKSMIVGVTSLADNEEERRAFMEGGLNHCLAKP 12                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 당         | 100.0%; Scor                                        | e 678; DB           | 10; Length 136;         |
| MATKSMGDIEKIKKKLNVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | S 1       | ilarity 100.0%;<br>Conservative 0;                  | No. 4.7e.           | Indels 0; Gaps          |
| MATKSMGDIEKIKKKLNYLIVDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGS SFDLILMDKEMPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKP SFDLILMDKEMPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKP SFDLILMDKEMPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKP                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |           | AATKSMGDIEKIKKKLNVLIVDDDP                           | LNLIHEKII           |                         |
| SFDLILMDKEMPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFWEAGLNHCLAKP                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 1         | MATKSMGDIEKIKKKLNVLIVDDDP                           | LNLIHEKII           |                         |
| SPOLILMDKEMPERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKP                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 61        | SFDLILMDKEMPERDGVSTTKKLRE                           | MEVKSMIVGV          |                         |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 21        | SPDLILMDKEMPERDGVSTTKKLRE                           | SMEVKSMIVGV         |                         |

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01-MAR-2003 (TrEWBLrel. 23, Last annotation update)
Hybrid histidine kinase DHKB.
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1951 QKPIKTSDILIQMI 1964
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2003 (TrEMBLrel. 23,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 35.8
Matches 48; Conservative
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                                                                                                                           SEQUENCE FROM N.A.
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Q8EZ63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MATKSMGDIEK----IKKKL-NVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVII
                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).

Bukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAINS-CV. Columbia;
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC TRK12 genomic sequence.";
Submitted (JAN-2001) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov Feldmann K.A., Flavell R.B., White O., Salzberg S.L.; Full-length messenger RNA sequences greatly improve genome annotation."; Genome Biol. 0:0-0(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
BEDYOFI V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
Feldmann K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 142;
                                                                                                                                                                                                                                     Putative response regulator protein (receiver component). T6K12.10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79.4%; Score 538; DB 10; Length 1 78.9%; Pred. No. 9.8e-40; rative 8; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Full Length cDNA from Arabidopsis thaliana.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; ARC16829; AAR26766.1; -.
EMBL; AY085638; AAM62859.1; -.
InterPro; IPR001789; Response_reg.
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Probom: PD000039; Response_reg; 1.
PROSITE: P550110; RESPONSE_REGULATORY; 1.
Phosphorylation: Sensory transduction.
SEQUENCE 142 AA; 15792 MW; 57487135FF2D5238 CRC64;
                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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                                                                                                                                                142 AA.
                                                                                                                                                                                    Created)
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                                                                                                                                                PRT;
                                       LTKDKIIPLINQLMDA 136
                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-MAR-2003 (TrEMBLrel. 23,
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Best Local Similarity
                 121
                                                                                                                                                                Q9M8Y4;
                                                                                                                                                Q9M8Y4
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015763
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Q9M8Y4
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1891 QMPEMDGFEATTAIRELEKSNLIESPPSKKHSHVVIVALTANSGYKDKQKCLSVGMNDFL 1950
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                                                                                                                                                                                                                                                                          A Linda M.J. Single Funned 37,0030,

A Linda M.J. Single Funned 37,0030,

A Linda M.J. Single Funned 37,0030,

The hybrid histidine kinase dhkB regulates spore germination in Dictyostellum discoldeum.";

Dev. Ball. 196.11-183 (1988).

Embl. AP024654; AAB71889.11,

Embl. AP003594; ATB1899.11,

InterPro; IPR004358; Bact_sens_pr_C.

InterPro; IPR004358; Bact_sens_pr_C.

InterPro; IPR004358; Bact_sens_pr_C.

InterPro; IPR004189; Response_reg.

InterPro; IPR00199; Response_reg.

InterPro; IPR00199; Response_reg; I.

Pfam; PR00512; HisRA; I.

Probom; PR000039; HarPase_C; I.

PRODOM; PR000039; HarPase_C; I.

RMART; SM00091; PAS; I.

SMART; SM00091; PAS; I.

RMART; SM00448; REC; I.

PROSITE; PS50109; HISRA; I.

PROSITE; PS50109; HISRA; I.

RNART; SM0048; RESPONSE_REGULATORY; I.

RNART; RNART; SM0048; RESPONSE_REGULATORY; I.

RNART; RNART; RNARTER RESPONSE_REGULATORY; I.

RNART; RNARTER RESPONSE_REGULATORY; I.

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Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
NCBI_TaxID=173;
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STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
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EMBL, AB011554; AAN51193.1; -.
Complete protecme.
SEQUENCE 820 AA; 94325 MW; 3DBE99966794E67D CRC64;
                                                         Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003 (TERMBLrel. 23, Last sequence update) Two-component hybrid sensor and regulator. LA3996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26.7%; Score 181; DB 5; 35.8%; Pred. No. 5.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29; Mismatches
Dictyostellum discoideum (Slime mold).
Eukaryota; Mycetczoa; Dictyostellida;
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                STRAIN=KAX3;
MEDLINE=98248997; Pubmed=9576830;
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RESULT 7
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                                                                                                                                                                                                                                                                                                                                           72 PERDGVSTTKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKIIPLIN 131
                                                                                                                                                                                                            DIILMDKEMPERDGVSTTKKLREMEVKS---MIVGVTSLADNEEERRAFMEAGLNHCLAK 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 IKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEM 71
                                                                                                                                                                    62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-288234, PubMed-1247157,
MEDLINE-2888234, PubMed-1247157,
MEDLINE-2888234, PubMed-1247157,
Melch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coll.";
Proc. Natl. Acad. Scil. U.S.A. 99:17020-17024(2002).
                                                                                                                                                                    8 DIEK----IKKKLNVLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSF
                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
NCBL_TaxID=217992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26.3%; Score 178.5; DB 16; Length 1197; 34.4%; Pred. No. 4.6e-07; Live 25; Mismatches 52; Indels 3;
                                DB 16; Length 820;
                                                                                              49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transferase; Complete proteome.
SEQUENCE 1197 AA; 134847 MW; 5088214E7F834F06 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 22, Last annotation update)
01-CT-2002 (TrEMBLrel. 22, Last annotation update)
CC3162.
CC3162.
Caulobacter crescentus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Sensor protein evgs precursor (EC 2.7.3.-).
                             ch 26.5%; Score 179.5; DB 1
1 Similarity 31.6%; Pred. No. 2.4e-07;
43; Conservative 29; Mismatches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        394 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                       120 PLTKDKIIPLINQLMD 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLD----LPILKSTLD 807
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Matches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EVGS OR C2906.
Escherichia coli 06.
                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1072 QL 1073
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09A3P0
                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
Q8CVU5
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                                                                                                                                                             SEQUENCE FROM N.A.

STRAIN=ATCC 1909 / CB15;

XX MEDIANE=21176989, PubMed=11259647;

XX Nierman W.C., Feldblymm T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

R Elsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

A POTOCKAI I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

A CALOMAY J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

A CLOMAY J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

A Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.,

T. Complete genome sequence of Caulobacter crescentus.";

Proc. Natl. Acad. Sci. U.S.A., 98:4136-4141(2001).

C -: SIMILARITY: THE N.TERMINAL REGION IS SIMILAR TO THAT OF OTHER

REGILATORY COMPONENTS OF SENSORY TRANSDUCTION SYSTEMS.

THERE, AE005980; AARX5124.1;

TIGR: COLSTAIRS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-OG:HI / CFT073 / ATCC 700928;
MEDLINE-22380244; Pubmed-12471157;
MEDLINE-23808244; Pubmed-12471157;
MEICH R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S. R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
Extensive mosaic structure revealed by the complete genome sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Gaps
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Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   transduction; Complete proteome.
Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
NCBL_TaxID=155892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 25.7%; Score 174; DB 16; Length 39-Best Local Similarity 31.7%; Pred. No. 3.1e-07; Matches 39; Conservative 31; Mismatches 49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003594; ATPbind_ATPase.
InterPro; IPR003567; His_kinase.
InterPro; IPR0010467; His_kinase.
InterPro; IPR001049; Response_reg.
If fam; Pr00072; response_reg; 1.
Pr00m; Pr00019; Response_reg; 1.
Ryn0039; Response_reg; 1.
RynART; SM00446; REC: 1.
RynART; RynOprorylation; Sensory transduction; Complete pr SEQUENCE 394 AA; 41592 MW; 6D9AF0B27BB70E70 CRC64;
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Last annotation update)
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01-MAR-2003 (TrEMBLrel. 23, Last s
Sensor protein rcsC (EC 2.7.3.-).
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SEQUENCE
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Q8ZGR4
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         SOUR REAL PROPERTY OF STREET OF STRE
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                                                                                                                                                                                                                                    18 VLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAV-IIHRDGGSSFDLILMDKEMPERDG 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 NVLIVDDDPLNLITHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDG
                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                             77 VSTIKKLREMEVKSMIVGVISLADNEEERRAFMEAGLNHCLAKPLIKDKI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas stutzeri (Pseudomonas perfectomarina).
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ol-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Sensor for ctr capsule biosynthesis, probable histidine kinase acting on RCSB.
RCSC OR 23477 OR ECS3107.
Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                       884 YRLTORIROLGLTLPVIGVTANALAEEKORC-LESGMDSCLSKPVTLDVI 932
                                                                                                                                                                                        in
                                                                                                                                    25.6%; Score 173.5; DB 16; Length 949; 33.6%; Pred. No. 9.7e-07; Live 35; Mismatches 33; Indels 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.5%; Score 173; DB 2; Length 417; 32.8%; Pred. No. 4e-07; ive 35; Mismatches 37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Graupher S., Wackernagel W.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ249741; CAB56474.1; ...
InterPro; IPR001570; Hpt.
InterPro; IPR001789; Response_reg.
Probom; PD000039; Response_reg; 1.
of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
EMBL. ASUG16763; AAN81215.1; -.
Transferase; Complete proteome.
SEQUENCE 949 AA; 106590 WW; DF8CA47F9EEB4088 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSTIE: PS50110; RESPONSE_REGULATORY; 1.
Kinase; Phosphorylation; Sensory transduction.
NON_TER 1 1 1 SEQUENCE 417 AA; 45749 MW; D196B4FFDDA23BB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        933 AA
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                                                                                                                                                               Best_Local Similarity 33.63
Matches 37; Conservative
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SMART; SM00448; REC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                            Query Match
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08XE39
1D 08XE
AC 08XE
DT 01.M
DT 01.M
DT 01.M
DE acti
GN RCSC
OS ESCH
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811 ILVVDDHPINRRLLADQLGSLGYQCKTANDGVDALNVL--SKNHIDIVLSDVNMPNMDGY 868
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SEQUENCE FROM N.A.
SETALINE-1156231; PubMed=11258796;
MEDLINE-21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Makino K., Ohnishi M., Kurokawa K., Marata T., Tanaka M., Tobe T., Isham T., Shiba T., Hattori M., Shinagawa H.; Takami N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Complete genomes esquence of enterohemorrhagic Escherichia coli Ol57H7 and genomic comparison with a laboratory strain K-12."; DNA Res. 8:11-22(2001).
EMBL: AR005464, AAG57353.1; -.
ESBL: AR005669; BAB365330.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of enterchaemorrhagic Escherichia coli O157:H7."; Nature 409:529-533(2001).
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
NCBI_TaxID=83334;
                                                                                                                                                                       STRAIN-OLD: HT / EDL933 / ATCC 700927;
MEDLINE-21074035; PubMed=11206551;
MEDLINE-21074035; PubMed=11206551;
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotcheck B.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Two component sensor kinase/response regulator protein RcsC (EC 2.7.3..) (Sensor for ctr capsule biosynthesis).
RCSC OR YPO1217 OR Y2971.
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33.9%; Pred. No. 1.4e-06;
live 32; Mismatches 37;
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PROSITE; PS50110; RESPONSE_REGULATORY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Interpro; IPR003594, Arbbind_Arpase.
Interpro; IPR004358; Bact_sens_pr_C.
Interpro; IPR003661; His_KinA.
Interpro; IPR005467; His_Kinase.
Interpro; IPR000144; PAS_domain.
Interpro; IPR001789; Response_reg.
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PLODOM; PD000039; Response_reg; 1.
SMART; SM00387; HATPase_c; 1.
SMART; SM00388; HISRS; 1.
SMART; SM0091; PAS; 1.
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Pfam; PF00512; HisKA; 1.
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                                                                                                                                                     SEQUENCE FROM N.A.
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Query Match
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STRAIN=KIM5 / Biovar Mediaevalis;

XX MEDIARE-21237863; Pubmed-12142430;

XX MEDIARE-21237863; Pubmed-12142430;

XA PREDIARE-21237863; Pubmed-12142430;

XA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,

XA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,

XA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,

A Genome sequence of Yersinia pestis KIM.";

XI Jacteriol. 184:4601-4611(2002).

REMBL, AGA14147; CAC90055.1;

YI Jacteriol. 184:4601-4611(2002).

REMBL, AGA18983; AAM86522.1;

REMBL, AGA18983; AAM86522.1;

REMBL, AGA18983; ARM86522.1;

RICEPPO: IPRO03564; ATPDING_ATPase.

RICEPPO: IPRO03561; His.Kinase.

RICEPPO: IPRO03789; Response_reg.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-21470413; PubMed-11586360; Parkhill J., Wen B. W., Thomson N.R., Titball R.W., Holden M.T.G., Parkhill J., Wen B. W., Thomson N.R., Titball R.W., Holden M.T.G., Barentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdenor-Tarraga A.M., Chilingworth T., Cronin A., Davies R.W., Davis P., Dougan G., Leather S., Moule S., Oyston P.C.F., Quail M., Ratlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Nature 413:523-527(2001).
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.3%; Score 171.5; DB 16; Length 957; 35.1%; Pred. No. 1.5e-06; ive 29; Mismatches 40; Indels 3;
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Vibrio fischeri.
Vibrio fischeri.
Sammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
NCBI_TaxID=668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Print's PR00072; response_reg; 1.
PRINTS. PR00344; BCTRLSENSOR.
Prodom: PD000039; RS-PORSE_reg; 1.
PROSITE; PS50109; HIS_KIN; 1.
Kinase; Transferase; Complete protecome.
SEQUENCE 957 AA: 108591 MW; 0447AllF59100011 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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Pfam; PF00512; HiskA; 1.
            Enterobacteriaceae; Yersinia
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Best Local Similarity 35.11
Matches 39; Conservative
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SEQUENCE FROM N.A.
                                                 SEQUENCE FROM N.A.
                         NCBI_TaxID=632;
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76 GVSTTKKLRE-MEVKSMIVGVTSLA----DNEEERRAFMEAGLNHCLAKPLTKDKIIPL 129
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"A two-component sensor required for normal symbiotic colonization of Euprymen scolopes by Vibrio fischeri.";
J. Bacteriol. 183:835-842(2001).
-: SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Gaps
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Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
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PROSITE; PS50110; PAS; 1.
PROSITE; PS50110; RESPONSE_REGULATORY; 1.
FROSINTE; PS50110; RESPONSE_REGULATORY; 1.
Kinase, Phosphorylation; Sensory transduction; Transferase.
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
NACOMPONENT SYSTEM SENSOR PROCESIN.
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33.9%; Pred. No. 1.6e-06;
iive 28; Mismatches 42.
                                                                                                                                                                                                                                                                                                                              EMBL; AF319618; AAG60694.1; -.
Interpro; IPR003594; ATPbind_ArPase.
Interpro; IPR003661; His_KinA.
Interpro; IPR003661; His_KinA.
Interpro; IPR003661; His_KinA.
Interpro; IPR003670; His_Kinase.
Interpro; IPR001610; PAC.
Interpro; IPR001010; PAC.
Interpro; IPR001010; PAS.
Interpro; IPR001014; PAS. domain.
Interpro; IPR001799; Response_reg.
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STRAIN=306 / ATCC 13902 / XV 101;
MEDLINE=22022145; PubMed=12024217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGRFAMS; TIGR00229; sensory_box; PROSITE; PS50109; HIS_KIN; 1. PROSITE; PS50113; PAC; 1.
MEDLINE=21142508; PubMed=11208780;
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Matches 43; Conservative
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
085663
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            A da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R., Auaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F., Adves L.M.C., Camargo L.E.A., Camarotte G., Cannavan F., Cardazo J., Chambergo F., Clapina L.P., R. Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H., Faria J.B., Ferreira R.C.C., Ferro M.I.T., R. Ferreira R.C.C., Gregio C.C., Gregio C.C., Gregio C.C., Ferro M.I.T., R. A connighieri E.F., Franco M.C., Gregio C.C., Gregio C.C., Ferro M.I.T., R. A tsuyyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos B.G.M., Lemos M. C., Ollveira V.R., Martine E.C., Machado M.A., Madelra A.M.B.N., Martinez-Rossi N.M., Martine E.C., Machado M.A., Madelra A.M.B.N., Mayki C.Y., Moon D.H., Prediati B.C., Machado M.A., Sena J.A.D., Silva C., de Souza R.F., Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F., Spinola L.A.F., Takita M.A., Tauffi D., Tsai S.M., White F.F., F. Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I. Spinola L.A.F., Ratingande dos Santos M., Truffi D., Tsai S.M., White F.F., Stubal J.C., Kitajima J.P., Raura S.M., White F.F., F. Setubal J.C., Kitajima J.P., Raura S.M., White F.F., Raura 417 459 463(2002).

R. Nature 417 459 463(2002).

R. InterPro: IPR003594; ArPbind_ATPase.

DR InterPro: IPR00566; His_kinase.

DR InterPro: IPR00566; His_kinase.

DR Ffam; PF00512; HisRA; I.

DR Ffam; PF00627; His_Kinase.

DR Ffam; PF00637; Response_reg; I.

DR Ffam; PF00637; Response_reg; I.

DR PRINTS; PS00109; HIS_KIN; I.

DR PRINTS; PS00109; HIS_KIN; I.

DR PRINTS; PS00109; HIS_KIN; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 KKLNVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPE 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               || : |:: | || :| :| || || 553 LDGYAATRRWRAMFTESGGRPVPIVAMTANAMAGDRERC-LAAGMDDYLSKPVAREQL 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74 RDGVSTTKKLREMEVKS-----MIVGVTSLADNEEERRAFMEAGLNHCLAKPLTKDKI 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-306 / ARCC 13902 / XV 101;
MEDLINB-22022145; PubMed=12024217;
da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
Quaggio R.B., Montelro-Vitorial C.B., Van Sluys M.A., Almaeida N.F.,
Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.Y.,
Faria J.B., Ferreira R.C.C., Ferreira R.C.C.,
Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xanthomonas axonopodis (pv. citri).
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
Xanthomonadaceae; Xanthomonas.
NCBI_TaxID=92829;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                769 AA; 83699 MW; B7995CA40A787593 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.1%; Score 170; DB 16; 30.5%; Pred. No. 1.5e-06; iive 38; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1364 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Two-component system sensor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 30.55
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete proteome. SEQUENCE 769 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8PJN8;
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RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

Ray Mactins E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

RA Martins E.C., Machado M.A., Madeira A.M.B.N., Matharia C.Y.,

RA Moreira L.M., NOVO M.T.M., OSULA J.N., Caliva C.Y., Oliveira W.C.,

RA Peraira H.A., Rossi A.M., Sena J.A.D., Silva C., de Souza R.F.,

RA Spinola L.A.F., Takita M.A., Tamira R.E., Takita B.F.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Spinola L.A.F., Takita M.A., Tamira R.E., Takita B.F.,

RA Spinola L.A.F., Rossi J.B.P.,

RA Spinola L.A.F.,

RA S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 VSTTKKLREMEVKSM--IVGVTSLADNEBERRAFMEAGLNHCLAKPLTKDKIIPLINQLM 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 NYLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Belas R., Schneider R., Melch M.; "Characterization of Proteus mirabilis precocious swarming mutants: identification of rsba, encoding a regulator of swarming behavior.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proteus mirabilis.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Proteus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ë,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24.7%; Score 167.5; DB 16; Length 1364; 29.2%; Pred. No. 5e-06; Live 37; Mismatches 45; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequ
01-MAR-2003 (TrEMBLrel. 23, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BB2000;
MEDLINE-99047557; PubMed-9829920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 29.29
Matches 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=584;
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Matches
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SEQUENCE FROM N.A.

SEQUENCE C 39913 / NCPPB 528;

MEDLINE=22022145; PubMed=12024217;

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almielda N.F.,

RA Alves L.M.C., do Amaral A.M., Destrollini M.C., Camargo L.B.A.,

RA Alves L.M.C., Connavan F., Carsino-Santos J.R., El-Dorry H.,

RA Caraclil R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Formighieri E.C., Mediado M.A., Madeira A.M.B.N., Martines Rossi N.M.,

RA Martins E.C., Mediado M.A., Madeira A.M.B.N., Martines Rossi N.M.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira V.R.,

RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

RA Setubal J.C., Kitajima J.P.,

RA Gendarison of the genomes of two Xanthomonas pathogens with differing R. Noats Specificities "."

RE Nature 417:459-463(2002).

RE EMBL, ABO12344; AAM41638.1; -.
                                                                                                                                                                                                                                                                                                                                                                        3
                                                                                                                                                                                                                                                                                                                                                                                                                     16 LNVLIVDDDPLNLIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERD 75
                                                                                                                                                                                                                                                                                                                                                                         Gaps
               -!- SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; (pv. campestris).
Xanthomonadacee; Xanthomonas.
NCBL_TaxID=340;
                                                                                                                                                                                                                                                                                                                                                                         3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        455 GYQLATTVRELSSTIPPIGVTANAIAEEKQRC-IDAGMNDCVSRPVS 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                           76 GVSTIKKLREMEVKSMIVGVTSLADNEEERRAFMEAGLNHCLAKPLT 122
                                                                                                                                                                                                                                                                                      Kinase; Phosphorylation; Sensory transduction; Transferase
                                                                                                                                                                                                                                                                                                                                                                        39; Indels
                                                                                                                                                                                                                                                                                                                   507 AA; 57326 MW; F5DA2EAD9C35DEF5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                           24.6%; Score 166.5; DB 2 36.4%; Pred. No. 1.9e-06; iive 26; Mismatches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1364 AA
                                                                                                                                                                                    PRINTS; PRO0344; BCTRLSENSOR.
SMARY; SM00387; HATPASe_C; 1.
SMART; SM00388; Hiska; 1.
SMART; SM00488; REC; 1.
PROSTIE; PS50110; RESPONSE_REGULATORY; 1.
                                                                  InterPro: IPR003594; ATPbind_ATPase. InterPro: IPR004358; Bact_sens_pr_C. InterPro: IPR004667; His_kina. InterPro: IPR001769; Response_reg. Ffam; PP02012; Harkh. IPR001789; Response_reg. Ffam; PP02012; Harkh. 1. PF0312; Harkh. 1. PF0312; Harkh. 1. PF0312; Harkh. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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   180:6126-6139(1998)
                                          EMBL; AF071215; AAC82662.1; -. HSSP; P06657; 2CHF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 36.4*
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
    Bacteriol.
                                                                                                                                                                                                                                                                                                       NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
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18 VLIVDDDPLNLIIHEKIIKAIGGISQTANNGEEAVIIHRDGGSSFDLILMDKEMPERDGV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24.1%; Score 163.5; DB 16; Length 1364; 30.3%; Pred. No. 1.1e-05; tive 36; Mismatches 44; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50112; PAS; 2.
PROSITE; PS50110; RESPONSE_REGULATORY; 2.
Complete Procedome.
SEQUENCE 1364 AA; 150167 WW; 49FIC5FBD9710316 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search completed: August 13, 2003, 19:12:15
Job time : 39 secs
                                                                                                                       InterPro; IPR000000; PAS_assoc_C.
InterPro; IPR00001014; PAS_domain.
InterPro; IPR001789; Response_reg.
Pram; PF02514; CHASE; 1.
Pram; PF02518; HATPase_C; 1.
Pram; PF00512; H15KA; 1.
IPR003594; ATPbind_ATPase.
IPR004358; Bact_sens_pr_C.
IPR006189; CHASE.
                                                                                                                                                                                                                                                                                                                                                                                           TIGRFAMS; TIGRO0229; sensory_box; PROSITE; PS50839; CHABE; 1. PROSITE; PS50109; HIS_KIN; 1. PROSITE; PS50113; PAC; 2.
                                                                 IPR003661; His_kinA.
IPR005467; His_kinase.
                                                                                                                                                                                                                                                                                   Pfam: PF00785; PAC; 2.
Pfam: PF00785; PAS; 2.
Pfam: PF00078; PSS; 2.
Pfam: PF00074; response_reg; 2.
PrINTS: PR00344; BCTRLSENSOR.
PrODOM; PD000039; Response_reg;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                          InterPro;
InterPro;
InterPro;
InterPro;
                                                                                                        InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
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#### US 099043890KP1



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Team: 1600PrintWorkingFolder

Dossier: 09904389

Legal Date: 10-25-2003

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|-------------|-----------------|
| 1 SRNT      | 94              |

Total number of pages: 94

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